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Human protein Sequ
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Drosophila melanog
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2 197	16	882	18	AAW34662	Partial PSD-93 pro
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9 180	15.	2466	21	AAY90272	
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2 176	<b>⊢</b> i •	1373	20	AAY04730	
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<b>*</b>	4	400	7	AAM3 3 2 3 0	numan polypeptide
				ALIGNMENTS	
RESULT 1 AAY29978					
82668	standard;	; Protein;	in;	233 AA.	
XX AC AAY29978;					
DT 23-NOV-1999	99 (first	st entry)	۲)		
DE Human cell	1 junction	PDZ	protein	ein CJPDZ.	
<pre>Human; c cancer; William'</pre>	ell junction neurological s syndrome.		PDZ prote disorder;	PDZ protein; PDZ domain; CJPDZ; d disorder; developmental disorder;	diagnosis; F;
AA OS Homo sapiens	ens.				
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Nucleic acids encoding cellular junction PDZ protein domains useful in

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Au-Young

Yue H,

WPI; 1999-561035/47, N-PSDB; AAZ21259.

(INCY-) INCYTE PHARM INC Patterson C,

98US-0151611 98US-0151611

11-SEP-1998; 11-SEP-1998;

US5958731-A. 28-SEP-1999. a

24-JUL-2001.

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The present sequence represents human cell junction PDZ protein (CJPDZ). CJPDZ polynucleotides and proteins may be used in the diagnosis, prevention and treatment of disorders associated with defective cell signalling. They may be used to treat cancers, neurological disorders and developmental disorders such as William's syndrome. CJPDZ or vectors cand developmental disorders such as William's syndrome. CJPDZ or vectors containing CJPDZ may be administered to treat any of the above diseases by rectifying mutations or deletions in a patient's genome that affect call signalling by expressing inactive proteins or to supplement the patients own production of CJPDZ protein domain.

Molecules may be administered to down regulate CJPDZ protein domain where said preventing their expression. CJPDZ protein domain their expression. CJPDZ protein domain their expression. CJPDZ protein duantitate the presence of similar inclinative therapy. They may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar need of restorative therapy. They may also be used to study the capparassion and function of CJPDZ protein domains and their role in capparation of antibodies and in assays to identify modulators of CJPDZ expression and activity.
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anti-leukaemic; neuroprotective; antiepileptic; anti-Alzheimer's disease;
nootropic; anti-convulsant; cancer; leukaemia; myeloma; sarcoma;
neurological disorder; epilepsy; Alzheimer's disease;
Huntington's chorea.
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the prevention, diagnosis and treatment of disorders associated with defective cell signalling such as cancers and neurological and
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                                                                    Claim 1; Column 39-40; 27pp; English.
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/label= PDZ_domain
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                                      developmental disorders
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Matches 233;
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The invention relates to a purified human cell junction PDZ (CUPDZ)

polypeptide. The polypeptide may be used as an antigen in the production
of antibodies against CUPDZ and in assays to identify molecules
which bind CUPDZ including modulators of CUPDZ expression and activity.
The anti-CUPDZ antibodies, agonists and antagonists may be used to
control/regulate expression and activity of CUPDZ. The anti-CUPDZ
antibodies may also be used as diagnostic agents for detecting the
presence of CUPDZ polypeptides in samples (e.g. by enzyme linked
immunoabsorbbat assay, ELISA). Disorders of cell signaling and CUPDZ
expression and activity that may be prevented, diagnosed and/or treated
by the above methods include, for example cancers (e.g. lenkaemia,
myelonm, sarroma or lung, liver, colon or spleen cancers), neurological
closeders (e.g. epilepsy, Alzheimer's disease and/or Huntington's
chorea). A full list of disorders that may be treated is given in the
specification. The present sequence represents human CJPDZ.
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                                                                                                                                                                                                                          Cellular junction PDZ proteins useful in the prevention, diagnosis and treatment of disorders associated with defective cell signalling such as cancers, neurological disorders and developmental disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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cell junction PDZ; CJPDZ; membrane-associated signalling protein;
signal transduction; postsynaptic density protein 95; PSD-95;
Drosophila lethal (1) discs large-1; Dlg; zonula occludens-1; ZO-1;
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Pred. No. 3.3e-108;
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100.0%; Pr
tive 0;
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                                  99US-0370102.
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                                                                                                       (INCY-) INCYTE GENOMICS INC
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N-PSDB; AAS11583.
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                                                                                                                                                                                                                                                                              William's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 AA;
                                  06-AUG-1999;
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The invention discloses a human cell junction PDZ (CUPDZ) polypeptide and the polynucleotide encoding it. PDZ is a conserved protein domain which was identified in various membrane-associated signalling proteins. These proteins couple activated receptors to downstream second messenger complex, multiprotein signal transduction pathways. PDZ domains were named after the three proteins they were first identified in postsynaptic density protein 95 (PSD-95), Drosophila lethal (1) discs large-1 (DJs) and souls occludens-1 (20-1). The polypeptides and polymucleotides can be used to diagnose or treat a disease or condition associated with decreased expression of functional CUPDZ, for screening compounds for effectiveness as agonists or antagonists, for screening compounds for effectiveness as agonists or antagonists, for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compounds that modulates the protein activity, for screening compounds for effectiveness in altering gene expression and for raising antibodies. The polypeptides and polypucclides are useful for the prevention, diagnosis and treatment of disorders associated with defective cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signalling such as cancers (e.g. leukaemia and lymphoma), neurological disorders (e.g. Alzheimer's disease and Parkinson's disease) and developmental disorders (e.g. muscular dystrophy and William's syndrome). The sequence presented is the human cell junction PDZ (CJPDZ) protein.
cell signalling; cancer; leukaemia; lymphoma; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cellular junction PDZ protein domains useful in the prevention, 'diagnosis and treatment of disorders associated with defective cell signaling such as cancers, neurological disorders and developmental
                     Alzheimer's disease; Parkinson's disease; developmental disorder; muscular dystrophy; William's syndrome.
                                                                                                                                                                      /note= "Putative PDZ domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders such as William's syndrome -
                                                                                                                             Location/Qualifiers
107..189
                                                                                                                                                                                                                                                                                                                                                                                                                                                Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 31pp; English.
                                                                                                                                                                                                                                                                                                                                       98US-0151611.
99US-0370102.
                                                                                                                                                                                                                                                                                               18-JUL-2001; 2001US-0909005.
                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Yue H, Au-Young J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABK87047
                                                                                                                                                                                                            US2002082388-A1
                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                       11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                          06-AUG-1999;
                                                                                                                                                                                                                                                   27 - JUN-2002
                                                                                                                                              Domain
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0; FCTAIREVYQYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGF 120 NVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKD 180 09 1 MEKPSVTSAPTADMATLTVVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSE 181 SVKLVVRYTPKVLEEMEARFEKLRTARRQQQQLLIQQQQQQQQQQQQQUHMS 233 ó ch 100.0%; Score 1170; DB 23; Length 233; ll Similarity 100.0%; Pred. No. 3.3e-108; 233; Conservative 0; Mismatches 0; Indels 0; 233 AA; Sequence 61 61 121 121 Query Match Best Local 3 Matches

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DB 22; Length 197; e-73; es 13; Indels

69.6%; Score 814; DB 22; 80.6%; Pred. No. 8e-73; live 24; Mismatches 13;

Query Match
Best Local Similarity 80.6
Matches 154; Conservative

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80

21 QPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLGSEFCTAIREVVQYMHETITVNG

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemmatopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or transmin.
                                                                                                                                                                                                Human, cytokine; cell proliferation, cell differentiation, gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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MANA: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides with cytokine-like activities,
Xu C, Car
R, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Asundi V, Zhou P,
Wang J, Zhang J, Ren F, Chen
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 3872-3873; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful in diagnosis and gene therapy
                                                                                     AA.
                                                                                   Protein; 197
                                                                                                                                                                       Human protein SEQ ID NO 1554.
                                                                                                                                                                                                                                                                                                                                                                                    2000US-0496914.
2000US-0560875.
2000US-0598075.
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2000US-0693325.
2000US-0728422.
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2000US-0654936.
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                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-476283/51.
                                                                                   AAM78892 standard;
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Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAK52025
                                                                                                                                                                                                                                                                                                 WO200157190-A2
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                                                                                                                                                                                                                                                                        Homo sapiens.
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01-SEP-2000;
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Zhao QA,
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Xue AJ,
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full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an Oilgo-dr primer and an Oilgonuclectide complementary

to the complementary strand of a polynuclectide which comprises one of

coligonuclectide comprises at least 15 nuclectides; or (b) a combination

of an Oilgonuclectide comprising a sequence complementary to the

complementary strand of a polynuclectide which comprises a 5'-end

complementary strand of a polynuclectide which comprises a 5'-end

complementary strand of a polynuclectide which comprises a 5'-end

complementary strand of a polynuclectide which comprises a 5'-end

complementary strand of a polynuclectide comprises a 5'-end

complementary strand of a polynuclectide comprises and the combination of

complementary strand of a polynuclectide comprises and the combination of

coligonuclectide which comprises at least 15 nuclectides and the combination of

the specification. The primer sets can be used in antisense therapy and

conditionally full-length cDNAs. The primers are also useful for the

conditionally full-length cDNAs. The primers are also useful for the

condetection and/or diagnosis of the abnormality of the proteins enceded by

the full-length cDNAs. The primers allow obtaining of the full-length

conditionally without any specialised methods. AAH13628 and
                          CPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPG 140
                                         EPVRLERDICRAIELLEKLQRSGEVPPQKLQALQRVLQSEFCNAVREVYEHVYETVDISS
                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                             GVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARF
                                                                                                                                                                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy
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, Otsuki 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                protein sequence SEQ ID NO:13038,
                                                                                                                                                                                                                     AAB93600 standard; Protein; 197 AA
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99JP-0300253,
2000JP-0118776.
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EKMRSAKRRQQ 196
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AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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                                                                                                                                                                                                                  81 CPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPG
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Wang 1
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Chen R,
                                                                                                                            69.6%; Score 814; DB 22;
80.6%; Pred. No. 8e-73;
iive 24; Mismatches 13;
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Zhang J, Ren F, C
I, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM79876 standard; Protein; 198 AA.
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Yang Y, Wejhrman T,
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200005-0598075
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200005-063561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                           Local Similarity 80.6
nes 154; Conservative
                                                      of the present invention
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EKMRSAKRRQQ 196
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N-PSDB; AAK53009.
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                                                                                        197 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157190-A2.
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27-APR-2000;
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19-JUL-2000;
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Zhao QA,
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allargy; anaemia; asthma; atherosclerosis; melanoma; Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer; glomerulonephritis; multiple sclerosis; Grave's disease; Osteoarthritis; osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma; arteriosclerosis; nootropic; anticonvulsant; antithyroid; nephrotropic; neuroprotective; dermatological.
                                                                                                                                                                                                                    Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                             7 EPVRLERDICRAIELLEKLORSGEVPPOKLOALORVIOSEFCNAVREVYEHVYETVDISS
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                                                                                                                                                                                                                                                                                                                                           DB 22;
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80.6%; Pred. No. 8.1e-73;
live 24; Mismatches 13
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/note= "SH3 domain"
93..174
/note= "PDZ domain"
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EKMRSAKRROO 197
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                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                    198 AA;
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                                                                                                                                                                                                                                                                                                    Sequence
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Best Local 3
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diffectiveness as an agonist or antagonist of XMAD. The Machan advances of a number of the XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonist or antagonist are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The gene for therapy to correct a genetic deficiency, to express a conditionally lethal gene product and to express a protein which affords protection against intracellular parasites and also for diagnosis of disorders associated with expression of XMAD. They are also used for generating hybridisation probes useful in mapping the naturally occurring genomic sequences and to create knock in humanised animals (pigs) or transgenic fragments derived from the polymucleotide sequences may be used as an increarry. Antibodies which specifically bind XMAD may be used for the diagnosis of disorders associated with the expression of XMAD, or in assays to monitor patients being treated with XMAD may also a microarray are also being treated with the expression of a microarray are also being treated with XMAD. Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune/inflammatory disorders such as acquired immune deficiency syndrome (ALDS), Addison's disease, allergies, anaemia, asthma, atherosclerosis, Crohn's disease, diabetes mellitus, atopic dermatitis, glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthritis, osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis, bacterial, fungal, parasitic, protozoal and helminthic infections and cell proliferative disorders such as actinic keratosis, arteriosclerosis and cancer including breast, bladder, bone marrow, brain and uterus cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 ETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                         New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, prevention, treatment of genetic, autoimmune and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosed, prevented or treated include genetic disorders such as adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's disease, myotonic dystrophy, sickle cell anaemia, thalassaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                       Azimzai Y, Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is a human extracellular matrix and cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.0%; Score 807; DB 22; 78.5%; Pred. No. 4.3e-72; ive 24; Mismatches 17;
                                                                                                                                                                   l P, Burford N, Azin
Shah P, Au-Young J;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 111-112; 135pp; English.
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                   05-DEC-2000; 2000WO-US32990.
                                                                                  99US-0172354
                                                                                                                         (INCY-) INCYTE GENOMICS INC.
                                                            99US-0172852
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Best Local Similarity 78.55
Matches 157; Conservative
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fR, Lu DAM,
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                                                          10-DEC-1999;
16-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                        disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for treating a PRO related disorder. The PRO polypeptides are useful for stimular, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of in gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colon cancer, breast tumour, prostate tumour, rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hundred and twenty two nucleic acids encoding PRO polypeptides, ful for treating a PRO related disorder and for diagnosing tumours
                                                                                                              Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Figure 76; 359pp; English.
                            AAU83629 standard; Protein; 207 AA.
                                                                                           Human PRO protein, Seg ID No 76.
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20000S-220605P-
20000S-220607P-
20000S-22064P-
20000S-220664P-
20000S-220664P-
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2000US-253646P.
2000WO-US32678.
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2000WO-US20710.
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2000US-0000000P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such as lung cancer,
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N-PSDB; ABK33573.
                                                                                                                                                                                      WO200208288-A2
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28-FEB-2001;
10-MAY-2001;
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25-JUL-2000;
26-JUL-2000;
28-JUL-2000;
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15-SEP-2000;
10-NOV-2000;
28-NOV-2000;
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                                                                     08-MAY-2002
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                                                                                                                                                                  Homo sapiens
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       RESULT 8
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weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO protein sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
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                                                                                                                                                                                                                                                                                                    59 DILDIIGSABIRAHATAKATVAAFTASEGHAHPRVVELPKTDEGLGFNIMGGKEQNSPIY
                                                                                                                                                                                                                                                                       14 MATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMH
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                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                    Length 207;
                                                                                                                                                                                                 Pred. No. 4.3e-72; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 17076
                                                                                                                                                                         69.0%; Score 807; DB 23;
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                                                                                                                                                                              Li PWD,
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                 157; Conservative
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N-PSDB; ABL07531.
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                                                                                                                          207 AA;
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Matches 157
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2000US-0225266
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14-AUG-2000;
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22-AUG-2000;
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23-AUG-2000;
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05-SEP-2000;
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08-SEP-2000;
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08-NOV-2000;
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                                                                                                                                                                                               81 CPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPG 140
                                                                                                                                                                                                                141 GVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARF 200
                                                                                                                                                                                                                                                                        specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                         21 QPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNG
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  printed
                                                                                                                0;
                                                                                     Length 195;
 The sequence data for this patent did not form part of the
                                                                                                                22; Indels
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                                                                                  64.4%; Score 754; DB 22; 77.9%; Pred. No. 7.6e-67; ive 20; Mismatches 22;
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19-MAY-2000; 2000US-0205515.
07-UNN-2000; 2000US-0214886.
28-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0215135.
07-JUL-2000; 2000US-021647.
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2000US-0186350.
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                                                                               Query Match
Best Local Similarity 77.99
Matches 148; Conservative
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DKQRNTRRRQ 195
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02-MAR-2000;
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11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
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04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 953; 880pp; English.
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(e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17083 represent novel signal transduction pathway protein, amino acid sequences of the invention.
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01-DEC-2000;
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17-NOV-2000;
                                                                                                                                                                         17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                        05-DEC-2000;
06-DEC-2000;
                                                                                                                                                                                             7-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM

WPI; 2001-465460/50. N-PSDB; AAS27316.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders

Claim 1; SEQ ID No 964; 880pp; English.

The invention relates to novel isolated polypeptides (I), and polypuclectides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ carappart rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g. Alzhelmer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal

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Claim 11;
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                             82 PEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 VAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 VADRHGGLKRGDQLLSVNGVSVEGEQHEKAVELLKAAQGSVKLVVRYTPRVLEEMEARFE 142
                                                                                                                                                                                                                                                                                                                                                                                                                       13 PHLQSLSLSQATVAAFTASEGHAHPRVVELPKTDEGLGFNIMGGKEQNSPIYISRVIPGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiamatory; antival; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; prollerative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bronching.
                    (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction pathway protein, amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                     Gaps
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disorders (e.g. glomerulonephritis), cardiovascular disorders
                                                                                                                                                                                                                                                                                                  Length 163;
                                                                                                                                                                                                                                                                                             49.5%; Score 579; DB 22; Length 1
84.1%; Pred. No. 1.6e-49;
Live 13; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ORFX ORF3128 polypeptide sequence SEQ ID NO:6256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB43364 standard; Protein; 150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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143 KMRSARRRQQHQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLRTARRQQQQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leach M;
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N-PSDB; AAC77573.
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; osteopathic; antiparkinsonian; nootropic; neuroprotective; cardiant; thrombolytic; coagulant; vasotropic; nmunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antiviral; antifungal; antirheumatic; antidiabetic; hypotensive; dermatological; antiviral; antirheumatic; antidiabetic; hypotensive; dermatological; antiviral; antirheumatic; antidiabetic; hypotensive; dermatological; or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy poliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, sythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic caneemia, burns, wounds, bone and cartilage damage, nocturnal heemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 KATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 KAIVAAFTASEGHAHPRVVELPKIDEGLGFNIMGGKEQNSPIYISRVIPGGVADRHGGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 RGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLRTARRRQ
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Novel nucleic acids and peptides derived from open reading frame
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 150;
                                  useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.1%; Score 575; DB 21;
90.2%; Pred. No. 3.6e-49;
11ve 8; Mismatches 4;
                                                                                                                                            Page 5443; 5507pp; English.
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99US-0134117.
99US-0134118.
99US-0160860.
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14-MAY-1999;
21-OCT-1999;
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12-MAY-2000; 2000WO-US13166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PL domain protein; leukocyte activation; synapse formation;
transmembrane neurotransmitter receptor; autoimmune disease;
transplantation rejection; inflammation; allergy;
inflammatory bowel disease; ulcerative collits; iletis; psoriasis;
asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a new method for modulating a biological function of an endothelial cell or hematopoietic cell. The method involves introducing into a cell, an antagonist that inhibits binding between a PDZ protein and a PL protein. The inhibitor is used to treat a disease mediated by hematopoietic cells, e.g. autoimmune disease. It may also be used to prevent transplantation rejection of a solid organ transplant. The method may also be used in the treatment of inflammation, allergy, inflammatory bowel diseases, ulcerative colitis, ineitis, psoriasis, asthma, atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis, graft rejection, transplantation rejection), atherosclerosis, cancers, infectious diseases, ischemia, vasulitis and Crohn's disease.
                                                                                                                                                                                                                                                                                                  Modulating a biological function of an endothelial cell or hematopoletic cell, useful for treating autoimmune diseases and infectious diseases, by administering an antagonist that inhibits binding between a PDZ protein and a PL protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endothelial cell; haematopoietic cell; PDZ domain protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 472; DB 22;
Pred. No. 3.6e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 VEGEHHERAVELLKAAKDSVKLVVRYTPKVLE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGEHHEKAVELLKAAKDSVKLVVRTTPKVLE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 28-43; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ischaemia; vasulitis; Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.3%; 5
                                         2000US-0176195.
2000US-0182296.
2000US-0196460.
2000US-0196527.
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                                                                                                                                                               (ARBO-) ARBOR VITA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                        WPI; 2001-080245/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 AA;
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                                            14-JAN-2000;
                                                                       14-FEB-2000;
                                                                                          11-APR-2000;
                                                                                                              11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-NOV-2000.
                      13-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92;
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                                                                                                                                                                                                            Lu PS;
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The present invention relates to a method for modulating a biological function of an endothelial cell or haematopoletic cell, comprises introducing into a cell an antagonist that inhibits binding between a por domain protein and a PL domain protein to result in inhibition of leukcoyte activation. The present sequence is a PDZ domain. PDZ domains of proteins are named after three prototypical proteins: PSD5.

Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain proteins are involved in synapse formation by organising transmembrane neurotransmitter receptors through intracellular interactions. The inhibitors identified by the present invention can be used to treat disease mediated by haematopoietic cells, e.g. autoimmune disease, inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthitis, multiple sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis, anteniamia, vasulitis and Crohn's diseases (e.g. viral infection), ischaemia, vasulitis and Crohn's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 HSHPRVVELPKTDEGLGFNVMGGKEQNSPIXISRIIPGGVAERHGGLKRGDQLLSVNGVS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibiting T cell-mediated response by hematopoietic cells, or for treating diseases characterized by inflammatory and humoral immune responses, e.g. inflammation, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New inhibitors of binding of a PDZ protein and PL protein for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endothelial cell; haematopoietic cell; PDZ domain protein;
PL domain protein; leukocyte activation; synapse formation;
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100.0%; Pred. No. 3.6e-39;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGEHHEKAVELLKAAKDSVKLVVRYTPKVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 30; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB58037 standard; Protein; 97 AA
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2000US-0182296.
2000US-0196460.
99US-0162498
99US-0170453
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Best Local Similarity 100.
Matches 92; Conservative
                                                                                                                                                                                                                                                                     (ARBO-) ARBOR VITA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-025003/03.
29-OCT-1999;
13-DEC-1999;
                                                                               14-JAN-2000;
                                                                                                              14-FEB-2000;
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inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis, ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic dematitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, insuln-dependent diabetes, Hashimoto diseases (e.g. viral infection), ischaemia, vasulitis and Crohn's diseases. The inhibitors can also be used to prevent transplantation rejection of a solid organ transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for modulating a biological function of an endothelial cell or haematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a PDZ domain protein and a PL domain protein to result in inhibition of leukcoyte activation. The present sequence is a PDZ domain. PDZ domains of proteins are named atter three prototypical proteins: PSDS, Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain proteins are involved in synapse formation by organising transmembrane neurotransmitter receptors through intracellular interactions. The inhibitors identified by the present invention can be used to treat a discasse mediated by haematopointic cells, e.g. autoimmune disease, inflammation and autoimmune disease.
                  transplantation rejection; inflammation; allergy; inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis; asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease; ischemnia; vasulitis; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating a biological function of a hematopoietic cell for treating an allergic response, or diseases mediated by immune system cells, comprises introducing into the cell a PDZ-PL interaction enhancer or inhibitor -
transmembrane neurotransmitter receptor; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 32; 143pp; English.
                                                                                                                                                                                                                                                                        14-MAY-1999; 99US-0134114.
14-MAY-1999; 99US-0134117.
14-MAY-1999; 99US-0134118.
21-OCT-1999; 99US-0162498.
13-DEC-1999; 99US-0170453.
14-JAN-2000; 2000US-0176453.
14-FEB-2000; 2000US-0195460.
                                                                                                                                                                                                                                       2000WO-US13205
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                                                                                                                     Homo sapiens.
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103 HSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVS 162 

163 VEGEHHEKAVELLKAAKDSVKLVVRYTPKVLE 194 VEGEHHEKAVELLKAAKDSVKLVVRYTPKVLE 92

Gaps 0;

Length 97; 0; Indels

40.3%; Score 472; DB 22; 100.0%; Pred. No. 3.6e-39; Live 0; Mismatches 0;

92; Conservative

Best Local Similarity Matches 92; Conserva

á g δ

Query Match

Search completed: September 23, 2003, 15:13:53 Job time: 47 secs

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PRIOR FILING DATE: 1936-09-15
PRIOR PELICATION DAMES: 1936-09-16
PRIOR PELICATION DAMES: 60/10048
PRIOR PELICATION NUMBER: 60/10049
PRIOR PELICATION NUMBER: 60/10019
PRIOR PELICATION NUMBER: 60/10147
PRIOR PELICATION NUMBER: 60/10147
PRIOR PELICATION NUMBER: 60/10147
PRIOR PELICATION NUMBER: 60/10141
PRIOR PELICATION NUMBER: 60/10141
PRIOR PELICATION NUMBER: 60/10141
PRIOR PELICATION NUMBER: 60/10141
PRIOR PELICATION NUMBER: 60/10196
PRIOR PELICATION NUMBER: 60/10649
PRIOR PELICATION NUMBER: 60/115559
PRIOR PELICATION NUMBER: 60/11573
PRIOR PELICATION NUMBER: 60/11575
PRIOR PELICATION NUMBER: 60/11573
PRIOR PELICATION NUMBER: 60/11577
PRIOR PELICATION NUMBER: 60/11577
PRIOR PELICATION NUMBER: 60/11577
PRIOR PEL
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74 ETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY 133 134 ISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193 14 MATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMH 5 Length 207; 17; Indels Score 807; DB 15; Pred. No. 2.1e-70; 24; Mismatches 17; PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR APPLICATION NUMBER: 60/144758
PRIOR PLING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/145698
PRIOR PELING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/146222
PRIOR APPLICATION NUMBER: 60/146222
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR FILING DATE: 1999-08-07
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR PILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR PILING DATE: 1999-08-17
PRIOR PELING DATE: 1999-10-09
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-06
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07 PRIOR APPLICATION NUMBER: 60/169835 EEMEARFEKLRTARRROOOO 213 24; 69.0%; 78.5%; FILING DATE: 1999-06-22 APPLICATION NUMBER: 60/: FILING DATE: 1999-06-22 157; Conservative Similarity 194 Query Match Best Local Matches Dp ρp ŏ g δŽ  $\delta$ 

Search completed: September 23, 2003, 15:24:25 Job time: 66 secs

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/ cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-227-884-76
US-10-227-884-76
US-10-129-819-19
US-10-218-631-76
US-10-218-631-76
US-10-218-631-76
US-10-218-49-76
US-10-227-883-76
US-10-227-883-76
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US-10-227-883-76
US-10-237-843-76
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US-10-237-843-76
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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US.10-219-464-76
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US.10-219-479-76
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ALIGNMENTS

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61 FCTAIREVYQYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGF
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                                    GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Patterson, Chandra
ITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
FILE REFERENCE: PF-0599 US
CURRENT APPLICATION NUMBER: US/09/909,005
CURRENT FILING DATE: 2001-07-18
PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 3
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Pred. No. 1.4e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
Sequence 1, Application US/09909005
Patent No. US20020082388A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
100.0%;
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Best Local Similarity 100.
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                   SOFTWARE: PERL Program SEQ ID NO 1 LENGTH: 233
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180

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APPLICANNI: WOOD, WILLIAM I.

TITLE OF INVENTION: SECRETED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC FILLS OF INVENTION: SECRETED AND TRANSHEMBRANE POLYPEPTIDES AND CURRENT FILLS OF INVENTION: SECRETED AND TRANSHEMBRANE POLYPEPTIDES AND CURRENT FILLS OF INVENTION: ACIDS ENCODING THE SAME CURRENT FILLS OF STATES: 2002-08-26
CURRENT FILLS OF DATE: 1997-019-460
PRIOR RELIGATION NUMBER: 60/059113
PRIOR RELIGATION NUMBER: 60/059113
PRIOR RELIGATION NUMBER: 60/05913
PRIOR RELIGATION NUMBER: 60/069873
PRIOR RELIGATION NUMBER: 60/069873
PRIOR RELIGATION NUMBER: 60/09910
PRIOR RELIGATION NUMBER: 60/09914
PRIOR RELIGATION NUMBER: 60/09919
                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
Wood, William I.
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APPLICATION NUMBER: 60/090691
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
FILING DATE: 1998-06-25
        179 EEMEARFEKMRSARRQQHQ 198
                                                                                                                                                               Sequence 76, Application US/10227884
Publication No. US20030027988A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                              Desnoyers, Luc
Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                      Goddard, Audrey
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APPLICANT: STEPDAO, JGEOTHER
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBENCE: P3530PLC3
CURRENT APPLICATION NUMBER: US/10/216,163
CURRENT PILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: (60/05913)
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: (60/062287)
PRIOR APPLICATION NUMBER: (60/062287)
PRIOR APPLICATION NUMBER: (60/063549)
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: (60/06387)
PRIOR PILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-03-25
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PRIOR PILING DATE: 1998-03-27
121 NYMGGKEQNSPIYISRIIPGGYAERHGGLKRGDQLLSYNGYSYEGEHHEKAVELLKAAKD 180
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                                                   181 SVKLVVRYTPKVLEEMEARFEKLRTARRRQQQQLLIQQQQQQQQQQQTQQNHMS 233
                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM.
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; Pred. No. 2.1e-70;
24; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul'J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
                                                                                                                                                                                                                                              Sequence 76, Application US/10216163
Publication No. US20030149239A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                             Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Homo Sapien
US-10-216-163-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Best Local Simil
Matches 157; (
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LENGTH: 207
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APPLICANT:
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| PRIOR FILMS DATE: 1999-10-12
| PRIOR PRICATION NUMBER: 60/12539
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THE APPLICATION NUMBER: 60/100385

RAPPLICATION NUMBER: 60/100390

RAPLICATION NUMBER: 60/100390

RELING DATE: 1998-09-15

RAPPLICATION NUMBER: 60/100647

RELING DATE: 1998-09-16

RELING DATE: 1998-09-18

RELING DATE: 1998-09-18

RELING DATE: 1998-09-17

RAPPLICATION NUMBER: 60/10019

RELING DATE: 1998-09-17

RELING DATE: 1998-09-27

RELING DATE: 1998-09-24

RELING DATE: 1998-09-24
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RAPPLICATION NUMBER: 60/101916

RAPLICATION NUMBER: 60/101922

RAPLICATION NUMBER: 60/101922

RAPLICATION NUMBER: 60/106178

RAPLICATION NUMBER: 60/106178

RAPLICATION NUMBER: 60/106248

RAPLICATION NUMBER: 60/10644

RAPLICATION NUMBER: 60/106464

RAPLICATION NUMBER: 60/106464

RETLING DATE: 1998-10-29

RAPLICATION NUMBER: 60/106464

RETLING DATE: 1998-10-30
                                                                     APPLICATION NUMBER: 60/090695
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/095302
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-08-26
APPLICATION NUMBER: 60/098544
FILING DATE: 1998-08-31
APPLICATION NUMBER: 60/099596
FILING DATE: 1998-09-09
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FILING DATE: 1998-08-04
APPLICATION NUMBER: 60/095916
FILING DATE: 1998-08-10
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FILING DATE: 1998-08-11
APPLICATION NUMBER: 60/096791
FILING DATE: 1998-08-17
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099816
FILING DATE: 1998-09-10
                               APPLICATION NUMBER: 60/090691
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/099811
FILING DATE: 1998-09-10
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FILING DATE: 1998-09-11
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APPLICATION NUMBER: 60/108849
FILING DATE: 1998-11-18
APPLICATION NUMBER: 60/112422
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APPLICATION NUMBER: 60/108787
FILING DATE: 1998-11-17
APPLICATION NUMBER: 60/108801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-09-09
             1998-06-24
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                                                   PRIOR
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APPLICANT: BAREA TO ANALY
APPLICANT: GENINGER, Juc.
APPLICANT: GOGGATI, FALLY
APPLICANT: WOOD, MILIAM I. I.
TITLE OF INVENTION: ACCESTED AND TRANSMEARANE POLYPEPTIDES AND NUCLEIC
CURRENN FILING DATE: 2002-04-08-38
CURRENN FILING DATE: 2002-04-08-38
CURRENN FILING DATE: 2002-04-08-38
CURRENN FILING DATE: 2002-04-08-38
CURRENT FILING DATE: 1997-10-28
FRIOR FILING DATE: 1997-10-28
FRIOR FILING DATE: 1997-10-28
FRIOR FILING DATE: 1997-10-28
FRIOR FILING DATE: 1998-04-25
FRIOR FILING DATE: 1998-04-26
FRIOR PALLOR THON WINDER: 60-008-33
FRIOR APPLICATION WINDER: 60-008-33
134 ISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193
                          US-10-230-163-76
Sequence 76, Application US/10230163
Publication No. US20030036635A1
GENERAL INFORMATION:
                                                                                                              APPLICATION NUMBER: 60/089905
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
                                                                                       EEMEARFEKLRTARRRQQQQ 213
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ETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY 133
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                                                                                              ISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BURFORD, Neil
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REFERENCE: PF-0760 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2,
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030044913A1 4062841CD1
US-10-149-819-19
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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
                                                                                                                                                                                                                                                                                         Sequence 19, Application US/10149819
Publication No. US20030044913A1
GENERAL INFORMATION:
                                                                                                                                                                     EEMEARFEKLRTARRQQQQ 213
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; Sequence 76, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YUE, Henry
APPLICANT: AZIMZAI, Yalda
APPLICANT: PATHG, Y TOM
APPLICANT: PATHG, Y TOM
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: SHAH, Purvi
APPLICANT: LAL, Preeti
APPLICANT: LAL, Preeti
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Best Local Similarity 78.5%;
Matches 157; Conservative
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                                                                                                                                                        R FILING DATE: 1999-01-12

R APPLICATION NUMBER: 60/115733

R APPLICATION NUMBER: 60/119549

R APPLICATION NUMBER: 60/119549

R FILING DATE: 1999-02-10

R PILING DATE: 1999-02-10

R FILING DATE: 1999-03-10

R PILING DATE: 1999-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R FILING DATE: 1999-07-28
R APPLICATION NUMBER: 60/146963
R FILING DATE: 1999-08-03
DR APPLICATION NUMBER: 60/149320
R FILING DATE: 1999-08-17
R APPLICATION NUMBER: 60/149638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R FILING DATE: 1999-04-27
R APPLICATION NUMBER: 60/131291
R FILING DATE: 1999-04-27
R FILING DATE: 1999-04-28
R FILING DATE: 1999-04-28
R APPLICATION NUMBER: 60/134287
R FILING DATE: 1999-05-14
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R APPLICATION NUMBER: 60/140723

R FILING DATE: 1999-06-22

R APPLICATION NUMBER: 60/141037

R APPLICATION NUMBER: 60/144758

R APPLICATION NUMBER: 60/144758

R APPLICATION NUMBER: 60/145698

R APPLICATION NUMBER: 60/145698

R FILING DATE: 1999-07-26
                  FILING DATE: 1998-12-22
APPLICATION NUMBER: 60/113605
FILING DATE: 1998-12-23
                                                                                       FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/115558
FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/127887
FILING DATE: 1999-04-05
APPLICATION NUMBER: 60/130232
FILING DATE: 1999-04-21
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FILING DATE: 1999-04-26
APPLICATION NUMBER: 60/131270
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APPLICATION NUMBER: 60/140650
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APPLICATION UNMARER: 60/151733
APPLICATION UNMARER: 60/164418
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APPLICATION NUMBER: 60/169495
FILING DATE: 1999-12-07
APPLICATION NUMBER: 60/169835
APPLICATION NUMBER: 60/113296
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FILING DATE: 1999-01-12
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APPLICATION NUMBER: 60/125775
FILING DATE: 1999-03-23
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FILING DATE: 1999-03-29
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APPLICATION NUMBER: 60/169445
                                                                      APPLICATION NUMBER: 60/113621
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APPLICATION NUMBER: 60/166361
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Matches 157; Conservative
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC14
CURRENT APPLICATION NUMBER: US/10/218,631
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: (0/059113
PRIOR APPLICATION NUMBER: (0/062287
PRIOR APPLICATION NUMBER: (0/062287
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
PRIOR FILING PAPELICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR FILING PAPELICATION NUMBER: 60/079656
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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
                                   Godowski, Paul'J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 EEMEARFEKMRSARRRQQHQ 198
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Best Local Similarity 78.54
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-10-230-414-76
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LENGTH: 207
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APPLICANT:
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wacd, william I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SEPREMENT: 2002-08-28
CURRENT APPLICATION NUMBER: US/10/30,338
CURRENT PILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/063287
PRIOR APPLICATION NUMBER: 60/063287
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07958
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07958
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07958
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07958
PRIOR FILING DATE: 1998-03-27
PRIOR PRI
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69.0%; Score 807; DB 15;
Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17;
                                                                                                                  Godowski, Paul'J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Publication No. US20030045687A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 EEMEARFEKLRTARRQQQQ 213
                             Desnoyers, Luc
Gerritsen, Mary
                                                                                        Goddard, Audrey
Baker, Kevin P.
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US-10-230-338-76
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC6
CURRENT APPLICATION NUMBER: US/10/216,159A
CURRENT FILING DATE: 2002-08-09
PRIOR PAPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/06213
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-18
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-28
PRIOR RELING DATE: 1997-10-28
PRIOR RELING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1998-03-05
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-27
PRIOR PRIOR APPLICATION NUMBER: 60/079556
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-27
PRIOR PRIOR PRICATION NUMBER: 60/079556
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.0%; Score 807; DB 15; 78.5%; Pred. No. 2.1e-70; ive 24; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEMEARFEKLRTARRQQQQ 213
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Gerritsen, Mary
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Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-216-159A-76
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US-10-218-849-76
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APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3530PIC98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 MATLIVVQPLILDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246
SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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69.0%; Score 807; DB 15;
Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17;
                                                                                                                                                                                                                                      CURRENT FILING DATE: 1930/LLO99
CURRENT FILING DATE: 2002-08-28
PRIOR PELING DATE: 2002-08-28
PRIOR PELING DATE: 2002-04-09
PRIOR PELING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065287
PRIOR APPLICATION NUMBER: 60/06549
PRIOR APLICATION NUMBER: 60/06973
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PILING DATE: 1997-10-31
PRIOR PELING DATE: 1997-12-17
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079286
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-25
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Sfathan, Jean-Philippe F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEMEARFEKLRTARRQQQQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-216-159A-76
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1998-03-27
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Stephan, Vetoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: WANDER: US/10/22/,873
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/062287
PRIOR APPLICATION NUMBER: 60/062287
PRIOR APPLICATION NUMBER: 60/063287
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                       14 MATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMH 73
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69.0%; Score 807; DB 15;
Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17;
           FILE REFERENCE: P3530P1C11
CURRENT APPLICATION NUMBER: US/10/218,849
CURRENT FILID DATE: 2002-08-12
FILE REFERENCE: DOS: 246
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 76
LENGTH: 207
TYPE: PRT
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 76, Application US/10227873 Publication No. US20030073816A1 GENERAL INFORMATION:
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079656
APPLICATION NUMBER: 60/079728
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-76
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R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/086392
R FILING DATE: 1998-05-22
R FILING DATE: 1998-06-17
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
R FILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R APPLICATION NUMBER: 60/090695
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/091982
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/095302
R FILING DATE: 1998-08-04
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FILING DATE: 1998-08-10
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FILING DATE: 1998-08-11
APPLICATION NUMBER: 60/096791
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APPLICATION UNMERS: 60/097986
APPLICATION DATE: 1998-08-26
APPLICATION NUMBER: 60/098544
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099816
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APPLICATION NUMBER: 60/101477
FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101738
FILING DATE: 1998-09-24
                                                                                               FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/084441
FILING DATE: 1998-05-06
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FILING DATE: 1998-06-18
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APPLICATION UNDBER: 60/099598
FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099803
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APPLICATION NUMBER: 60/100919
                                               FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/085579
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/099596
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FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/100390
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APPLICATION UNMBER: 60/100627
FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100848
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APPLICATION NUMBER: 60/090691
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FILING DATE: 1998-04-15
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                                                                                            1998-04-22
                           APPLICATION NUMBER:
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R FILING DATE: 1998-11-17
R APPLICATION NUMBER: 60/108849
R FILING DATE: 1998-11-18
R APPLICATION NUMBER: 60/11242
R FILING DATE: 1998-12-15
R APPLICATION NUMBER: 60/113296
                                                                                                                                                                                                                      A APPLICATION NUMBER: 60/106464
A FILING DATE: 1998-10-30
A APPLICATION NUMBER: 60/106905
A PILING DATE: 1998-11-03
A APPLICATION NUMBER: 60/108787
A FILING DATE: 1998-11-17
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R FILING DATE: 1999-03-19
R APPLICATION NUMBER: 60/125775
R FILING DATE: 1999-03-23
R APPLICATION NUMBER: 60/126773
R APPLICATION NUMBER: 60/126773
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R APPLICATION NUMBER: 60/127887
R FILING DATE: 1999-04-05
R FILING DATE: 1999-04-21
R APPLICATION NUMBER: 60/131022
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APPLICATION NUMBER: 60/144758
FILING DATE: 1999-07-20
APPLICATION NUMBER: 60/101741
FILING DATE: 1998-09-24
APPLICATION NUMBER: 60/101786
FILING DATE: 1998-09-25
APPLICATION NUMBER: 60/101916
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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/115733
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APPLICATION NUMBER: 60/119549
FILING DATE: 1999-02-10
APPLICATION NUMBER: 60/123618
FILING DATE: 1999-03-10
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APPLICATION NUMBER: 60/131270
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APPLICATION NUMBER: 60/131291
FILING DATE: 1999-04-27
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APPLICATION NUMBER: 60/140650
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APPLICATION NUMBER: 60/140723
FILING DATE: 1999-06-22
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APPLICATION NUMBER: 60/113605
FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/113621
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APPLICATION NUMBER: 60/146963
                                                                                            APPLICATION NUMBER: 60/101922
FILING DATE: 1998-09-24
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APPLICATION NUMBER: 60/134287
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FILING DATE: 1998-10-28
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119 ISRVIPGGVADRHGGLKRGDQLLSVNGVSVEGEQHEKAVELLKAAQGSVKLVVRYTPRVL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 MATLIVVOPLITEDRDVARAIELLEKLOESGEVPVHKLOSLKKVLOSEFCTAIREVYQYMH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 ETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY
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CURRENT APPLICATION NUMBER: US/10/227,883
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: U0/119,480
PRIOR PELING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-18
PRIOR FILING DATE: 1997-10-18
PRIOR FILING DATE: 1997-10-31
PRIOR PELICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR PELICATION NUMBER: 60/069873
PRIOR PELING DATE: 1997-12-17
PRIOR PELING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FLING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
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PRIOR APPLICATION NUMBER: 60/164418
PRIOR APPLICATION NUMBER: 60/164418
PRIOR PILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-09
PRIOR PAPLICATION NUMBER: 60/16945
PRIOR FILING DATE: 1999-12-07
PRIOR PAPLICATION NUMBER: 60/16945
PRIOR FILING DATE: 1999-12-07
PRIOR PAPLICATION NUMBER: 60/16945
PRIOR FILING DATE: 1999-12-07
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Vean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Modd, William II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 EEMEARFEKLRTARRQQQQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 EEMEARFEKMRSARRRQQHQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 76, Application US/10227883 Publication No. US20030073817A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 78.5%
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desnoyers, Luc
Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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Sequence 16, Application US/09100804

Patent No. 6066472

GENERAL INFORMATION:

APPLICANT: GONEZ, LEONEL JORGE

APPLICANT: SARAS, JAN

APPLICANT: CLAESSON WELSH, LENA

APPLICANT: CLEESSON WELSH, LENA

APPLICANT: HELDIN, CARL-HERRIK

TITLE OF INVENTION: EXPRESSION OF UNCLEOTIDE SEQUENCES FOR NOVEL PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                     106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                        Gaps
                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Sequence
US-09-562-737-27
                                                                                                                                                                                               1;
                                                                                                                                 Query Match
Best Local Similarity 39.4%; Pred. No. 7.8e-09;
Matches 37; Conservative 18; Mismatches 38; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OFTANTING SISIEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
FILING DATE:
CLASSIFICATION
FILING APPLICATION
FILING APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-804-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-82P-1993
FILING DATE: 01-82P-1993
FILING DATE: 01-82P-1993
FILING DATE: 01-82P-1993
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-82P-1994
ATORNEY-AGENT INFORMATION:
NAME: GATES, EDWARD R.
REFERENCE/DOCKET NUMBER: 31,616
REFERENCE/DOCKET NUMBER: 31,616
REFERENCE/DOCKET NUMBER: 10461/7003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEAR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 600 ATLANTIC A CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: USA ZIP: 02210
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TELEFAX: 617-720-2441
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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US-09-100-804-16
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US-09-100-804-16
FEATURE:
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September 23, 2003, 15:13:08; Search time 17 Seconds (without alignments) 579:908 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                            328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                              US-09-909-005-1
                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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Description	ì	<u>,</u>	m o	n i		'n		m	Seguence 30, Appl	12,	-	2, 2	3,		16,	28,	23,	54,	54,		29,		25,	51,	28,	H	Sequence 1, Appli
ΙD	-151-611	707-	US-09-151-611-3	US-09-3/0-102-3	US-09-562-737-2I	US-09-233-086-3	US-08-596-291-3	ι	US-09-562-737-30	US-09-080-855-12	US-09-566-076-12	PCT-US94-09943-2	US-09-306-998-3	US-09-562-737-27	US-09-100-804~16	US-09-562-737-28	US-09-562-737-23	US-08-545-860D-54	PCT-US94-04496-54	0	-09-562-737-2		US-09-562-737-25	US-09-562-737-51	US-09-100-804-28	-08-410-	US-08-259-514-1
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% Query Match	100.0	T00.0	υ. υ.	55.0	16.8		15.7	15.7	15.4	15.4	15.4	15.4	14.9	14.8	14.7	14.7	14.6	14.6	14.6	14.4	14.4	14.1	13.8	13.5	13.4	13.4	13.4
Score	1170	0/17	543.5	543.5	196.5	190	184	184	180.5	180,5	180.5	180.5	174.5	173.5	172.5	172.5	171	170.5	170.5	169	168.5	164.5	161.5	•		156.5	156.5
Result No.	П	71	v) •	ქ* ს	ν,	ا ف	7	8	ወ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

RESULT 2 US-09-370-102-1 : Sequence 1, Application US/09370102 : Patent No. 6265547

GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice

Sequence 1, Appli Sequence 25, Appli Sequence 2, Appli Sequence 17, Appli Sequence 24, Appl Sequence 22, Appl Sequence 21, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 25, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 26, Appli		KKK C G G C C C C C C C C C C C C C C C	00000000000000000000000000000000000000
US-08-858-311-1 US-09-100-804-25 US-09-100-804-25 US-09-140-2 US-09-147-119-7 US-09-147-119-7 US-09-562-737-24 US-09-966-243-219 US-09-562-737-22 US-09-562-737-22 US-09-562-737-56 US-09-562-737-56 US-09-562-737-57 US-09-140-14 US-09-140-087-27 US-09-140-53 US-08-4496-53 US-08-665-067-2	ALIGNMENTS	a WCTION PDZ PROTEIN US/09/151,611 9-11 0-11 0-11 0-11 0-11 0-11 0-11 0-	SVKLVVRYTPRVLEERRARFEKLRTARRQOOQLLIQQOOQQOQQQQQQQQOMS 
13.4 13.3 13.2 13.2 13.2 12.9 12.9 12.6 12.6 12.6 12.6 12.6 12.6 12.6 12.6 12.6 12.6 12.9		ULT 1  09-151-611-1  atent No. 5958731  atent No. 5958731  atent No. 5958731  APPLICANT: Yue, Henry  APPLICANT: Au-Young, Janice  APPLICANT: Au-Young, Chandra  TITLE OF INVENTION: CELL JUNCTION  FILE REFERENCE: PF-0599 US  CURRENT FILING DATE: 1998-09-11  CURRENT FILING DATE: 1998-09-11  NUMBER OF SEQ ID NOS: 3  SOFTWARE: PERL Program  LENGTH: 233  TYPE: FRY  ORGANISM: Homo sapiens  FRATURE: OTHER INFORMATION: 1974337  09-151-611-1  I MLKPSVTSAPTADMATITVVQPI  I MLKPSVTSAPTADM	ω ω
28 156 156 156 156 156 156 156 156		SISTED SI CHE	Qy 181 Db 181

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MEDITAR=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Worthan J.R., Yandell M.D., Chang M., Pfelifer B.D.,
RA Brandon R.C., Rogers Y.H., Blazel R.G., Change M., Pfelifer B.D.,
RA Brandon R.C., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Bortkova D., Botchan M.R., Bouck J., Brokstein P., Enotter P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Bodson K., Doup L.E., Downes M., Dugarn-Rocha S., Pleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Reriera S., Fleischmann W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 GVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARF 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 SHDVRASATAKATVAAFAASEGHAHPRVVELPKTEEGLGFNVMGGKEQNSPIYISRIIPG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 QPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNG 80
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Xao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.W., Zhong W., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
Science 287:2185-2195(2000).
SEMEL, AREO3750; ARE56389.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                        64.4%; Score 754; DB 5; Length 195; 77.9%; Pred. No. 8.3e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                195 AA; 21493 MW; EF9DF5ED71A73FBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TIEMBLIel. 23, Created)
01-MAR-2003 (TIEMBLIel. 23, Last sequence update)
01-MAR-2003 (TIEMBLIel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       77.9%; Pred. N.
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                                                                                                                                                                                                       Flybase; FBGn0039269; veli.
InterPro; IPR004172; L.27.
InterPro; IPR004478; PDZ.
Pfam; PF02828; L.27; 1.
SMART; SM00569; L.27; 1.
SMART; SM00569; L.27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 148; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 DKQRNTRRRQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                          HSSP; Q12959; 1PDR
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Rd Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris M.L., Barrey D., Heiman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Lasko P., Lei Y., Leit Y., Leit Y., Lioth D., Lai Z., Liang Y., Lin X., Markei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Morn K., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Reinert K., Kemington K., Saunders R.D., Scheeler F., Shen H., Spier E., Siden-Kiamos I., Simpson M., Strong R., Sun E., Santh T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Ra Zheng X.H., Zahori J.S., Zhan M., Zhang G., Zhao G., Zhao G., Zhao G., Zhao X., Smith H.O., Rhan P., Shan M., Zhang W., Zhao X., Zhao X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Brans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A carison J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Rerriera S., Prise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Lip P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A Pacleb J., Parzagas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittan G.S., Patel S., Pfeiffer B.,
A Stapleton M., Strong R., Syirskas R., Tector C., Tyler D.,
A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of Drosophila malanogaster genome.";
Submitted (MAR-2000) to the EMBL/Genbank/PDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 QPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNG
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; Pred. No. 5.2e-48;
20; Mismatches 24; Indels 53; Gaps
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Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Misra S., Crosby M.A., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
"Annotation of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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85 RARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAE 144
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                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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Caenorhabditis elegans.
Eukaryota: Metazoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE=96200771; PubMed=8612272;
MEDLINE=96200771; PubMed=8612272;
Simske J.S., Kaech S.M., Harp S.A., Kim S.K.;
LSTT-23 receptor localization by the cell junction protein LIN-7 during C. elegans vulval induction.",
Cell 85:195-204(1996).
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                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C.elegans: A platform for
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                                                                                                                                                                           Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1999).
-!- SIMILARITY: COWTAINS 1 PDZ/DHR DOMAIN.
EMBL; AL034488; CAA22459.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 1 PD2/DHR DOMAIN.
EMBL; U78092; AAB36684.1; -.
HSSP; Q12959; 1PDR.
                                                                                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, Q12959; IPDR.
WormPep; Y54G11A.10; CE28370.
InterPro; IPR004412; L27.
InterPro; IPR001478; PDZ.
Pfam; PF0328; L27; 1.
Pfam; PF03595; PDZ; 1.
SMART; SM03659; L27; 1.
SMART; SM03659; L27; 1.
SMART; SM0328; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
SEQUENCE 316 AA; 35663 MW;
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InterPro; IPR001478; PDZ
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Caenorhabditis elegans.
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                                                                                                                       SEQUENCE FROM N.A.
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P90976;
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                                                                                                                                            44 EVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNGCPEFRARATAKATVAAFAASEGH 103
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O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 19.0 kDa protein (Fragment).
Schistosoma mansoni (Blood fluke).
Enkaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomat
                    -GLGFNVMGGKEQNSPIYISRIIPGGVAERHGGL
                                                                                                               KRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLRTARRR
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MEDLIRE-99334538; PubMed=10406037;
Harrop R., Coulson P.S., Wilson R.A.;
"Characterization, cloning and immunogenicity of antigens released by lung-stage larvae of Schistosoma mansoni.";
Parasitology 118:583-594(1999).
-!-SIMILARIPT: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL; AF030965; AAB86566.1; --
HSSP; P31016; 1BFE.
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Last annotation update)
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InterPro; IPR001478; PDZ.
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PROSITE; PS50106; PDZ; 1.
Hypothetical protein.
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Pfam; PF00595; PDZ; 1.
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SEQUENCE
               117
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Q9U245;
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                                                                                                                                                 Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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ESCURENCE FROM N.A. Firestein B.L., Rongo C.; Firestein B.L., Rongo C.; Millar to SAP97 and is required for adherens
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                                                                                                                    Length 297;
                                                                       297 297
297 AA; 33580 MW; A8F15EDB90B0A90E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-MAR-2003 (TIEMBLrel. 23, Last annotation update)
MAGUK protein DLG-1 (SAP97-like protein DLG-1).
                                                                                                                    DB 5;
                                                                                                               Query Match 55.0%; Score 643.5; DB 5. Best Local Similarity 70.6%; Pred. No. 1.5e-44; Matches 127; Conservative 29; Mismatches 23.
                                                                                                                                                                                                                                                                                                                                                                                     967 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        junction formation.";

Mol. Biol. Cell 0:0-0(2001).
-!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
EMBL, AJ295228; CAC35153.1;
EMBL; AF406786; AAL01376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodom; PD000066; SH3; 1.
SMART; SM0072; Gukc; 1.
SMART; SM00569; L27; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50055; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; Q12959; IPDR.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR004172; L27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004172; L27.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PDZ; 3.
Pfam; PF00018; SH3; 1.
Pfam; PF02828; L27; 1.
Pfam; PF00595; PDZ; 1.
SMART; SM00269; L27; 1.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=N2;
                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   09BI79
                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                       09BI79
  DR DR DR SO FIT SO
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106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                             1;
                                                                Length 967;
                                                                                             Indels
                                 967 AA; 106991 MW; 44CDF119D6C6B368 CRC64;
                                                                                                                                                                                                   166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                           ch 20.0%; Score 233.5; DB 5;
1 Similarity 48.5%; Pred. No. 2e-10;
48; Conservative 18; Mismatches 32;
                                                                                                                                                                                                                                                          completed: September 23, 2003, 15:14:58 le : 42 secs
PROSITE; PS50002; SH3; 1.
                                                             Query Match
Best Local Similarity
               SH3 domain.
                                 SEQUENCE
                                                                                           Matches
                                                                                                                                                                                                                                                          Search co
   S KW
                                                                                                                                                    g
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GenCore version 5.1.6 copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 23, 2003, 15:11:58; Search time 37 Seconds Run on:

(without alignments)
1625.034 Million cell updates/sec

US-09-909-005-1 1170

1 MLKPSVTSAPTADMATLTVV......LLIQQQQQQQQQQQQTQONHMS 233 Perfect score: Sednence:

Scoring table:

Gapop 10.0 , Gapext 0.5 BLOSUM62

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_23:\* Database :

sp\_archea:\* sp\_bacteria:\*

sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_unclassified:\* sp\_vertebrate:\* sp\_mhc:\*
sp\_organelle:\*
sp\_phage:\* sp\_plant:\* sp\_rodent:\* sp\_rvirus:\* sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_bacteriap:\*

sp\_archeap:\*

# SUMMARIES

Description	Ol4910 homo sapien	Q9z250 rattus norv	Q8jzs0 mus musculu	Q9nup9 homo sapien	088952 mus musculu	088951 mus musculu	Q92252 rattus norv	Q9hap6 homo sapien	Q9z251 rattus norv	Q9vby7 drosophila	Q8imt8 drosophila	017458 schistosoma	Q9u245 caenorhabdi	P90976 caenorhabdi	Q9bi79 caenorhabdi	Q18165 caenorhabdi
ID	014910	092250	Q8JZS0	O9NUP9	088952	088951	092252	Q9HAP6	092251	Q9VBY7	QBIMTB	017458	090245	P90976	Q9BI79	018165
DB	4	11	11	4	11	11	11	4	11	Ŋ	ιΩ	Ŋ	S	J.	Ŋ	Ŋ
% Query Match Length DB	233	219	211	197	197	207	207	207	182	195	244	171	316	297	196	1064
% Query Match	100.0	92.1	90.3	9.69	9.69	69.1	69.1	0.69	64.8	64.4	58.5	55.4	55.3	55.0	20.0	20.0
Score	1170	1077.5	1057	814	814	808	808	807	758	754	684.5	648.5	647.5	643.5	233.5	233.5
Result No.	П	(7)	ო	4	2	9	7	80	0	10	11	12	13	14	15	16

291xm9 mus musculu 29vyz4 drosophila 29vyz5 drosophila 29vyz6 drosophila 29vz1 mus musculu 29z0r1 mus musculu 29bt1 mus musculu 2969u8 homo sapien 29hdz6 homo sapien 29rd1 mus musculu 29cqn7 mus musculu 29cqn7 mus musculu 29cqn7 mus musculu 29cqn7 mus musculu 20cqn7 mus musculu	Q921X3 mus musculu Q921X3 mus musculu Q800H8 mus musculu Q8Vby6 mus musculu Q8Vby5 mus musculu Q8Vby5 mus musculu Q8Vby6 mus musculu Q8Vby6 mus musculu Q8Vby6 mus musculu Q8Vby8 mus musculu Q9Vby3 prachydanio	Vector musculu Q8k4t6 rattus norv Q8k4v4 rattus norv Q21075 caenorhabdi Q28006 bos taurus Q9w466 drosophila Q43798 homo sapien Q8n790 homo sapien Q8n791 homo sapien
Q91XM9 Q9VZ4 Q9VZ5 Q9VZ5 Q9BSV4 Q9ET11 Q8EH60 Q9EH0 Q9EH0 Q9HD26 Q9HD26	Q921K3 Q8C0H8 Q8VBY0 Q8VBY0 Q8VBY5 Q8VBX5 Q8VBX6 Q55164	Q05402 Q08K4T6 Q021075 Q21075 Q19846 Q19846 Q9W486 Q43798 Q8N790 Q6WX31
	205 2055 2055 20055 20055	7 7
13.0 17.1 17.1 17.1 17.1 17.1 17.0 16.8		11111111111111111111111111111111111111
219 208.5 208.5 199.5 199.5 198.5 198.5 198.5 198.5	1887.55 1887.55 1887.55 1887.55 186.55	185 178.5 178.5 176.5 176.5 176 174.5 174.5
20000000000000000000000000000000000000	00000000000000000000000000000000000000	v w w w 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

### ALIGNMENTS

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MEDLINE—99274724; PubMed=10341223;
JOK., Derin R., Li M., Bredt D.S.;
JoK., Derin R., Li M., Bredt D.S.;
"Characterization of MALS/Vells-1, -2, and -3: a family of mammalian arbaracterization of MALS/Vells-1, -2, and -3: a family of mammalian postsynaptic density-95/NWDa receptor postsynaptic complex.";
J. Neurosci. 19:4189-41991999).
J. Neurosci. 19:4189-41991999).
EMBL, AF038826; AAB84251.1; -
EMBL, AF038826; AAB84251.1; -
EMBL, AF123881; AAD48500.1; -
HSSP, Q12933; 3PpZ.
Genew; HGNC:17787; LIN7A.
                                                                                                                                                                                                                                                                             Butz S., Okamoto M., Sudhof T.C., Atripartite protein complex with the potential to couple synaptic vesicle exceptosis to cell adhesion in brain."; cell 94:773-782(1998).
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 32-233 FROM N.A. AMOS 28 & CO
Rousset R., Fabre S., Desbois C., Bantignies F., Jalinot P.,
Oncogene 15:0-01997).
[3]
                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
1-JAN-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VELI 1 (TAX interaction protein 33) (Fragment).
                                                                                                                                                                                                                                                                                                                                                AF628826
                                   233 AA.
                                   PRT;
                                                                                                                                                                                                                                                   TISSUE=Testis;
MEDLINE=98424246; PubMed=9753324;
                                   PRELIMINARY;
                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                 014910
                                                                                                                                  MALS-1
RESULT 1
               014910
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us-09-909-005-1.rpr

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 23, 2003, 15:12:28; Search time 18 Seconds (without alignments) 1244.850 Million cell updates/sec Run on:

US-09-909-005-1 Perfect score:

1170 1 MLKPSVTSAPTADMATLTVV......LLIQQQQQQQQQQQQQUHMS 233 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\* Database :

pir1:\*
pir2:\*
pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		U	channel associated	discs-large tumor	synapse-associated	postsynaptic densi	postsynaptic densi	homolog of Drosoph	synapse-associated	homolog of Drosoph	multiple PDZ domai	multi PDZ domain p	hypothetical prote			protein-tyrosine-p	protein-tyrosine-p	tyrosine phosphata			brain-specific and	protein-tyrosine-p	atypical protein k	hypothetical prote				0
SUMMARIES	QI	T27179	T15617	T10811	G01974	A39651	A45436	JH0800	T09599	138757	I56552	I38756	T30259	T46612	T23160	T16191	S71625	167629	167630	I81209	I81210	T42372	JE0209	5497	T13948	2134	T28036	57	ø	29
	DB	7	~	~	a	Н	N	N	7	~	7	7	~	~	~	7	7	C3	~	7	7	7	7	Н	~	N	~	7	~	7
	Length	317	1131	852	870	960	720	724	767	904	911	926	2055	2054	1012	431	2450	2466	2294	117	126	1171	1256	2490	1337	578	390	423	440	538
8	Match	ø	0	$\infty$	œ	17.8	ø	16.8	ė.	ġ,	o	Ø	ø	S	S	S	4	14.7	14.4	4	4	4	14.1	4	13.8	13.6	m	B	13.2	12.9
	Score	662	233.5	219	217.5	208.5	196.5	196.5	196.5	192	192	192	191.5	186.5	177	176	173.5	172.5	169	167.5	167:5	165	165	165	161	٦	154.5	54	54	151
+ 2000	NO.	Н	63	m	4	S	9	7	ထ	D	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

numb-binding prote	AMPA glutamate rec synaptic scaffoldi	PSD-95-related pro	dystrophin-associa	syntrophin-1 - mou	alpha-syntrophin -	eye development pr	tyrosine kinase ac	hypothetical prote	protein co-factor	neurabin - rat	hypothetical prote	hypothetical prote
T09458 T09457	T32733 T14152	S60315	A53214	184771	S62894	A56158	G01158	T00346	I46532	T43275	T20145	119630
2 2	~ ~	2.0	0	N	~	7	~	7	7	N	~	
628	1112	87	505	503	505	1893	450	1281	358	1095	2172	624
12.9	12.9	12.9	12.6	12.5	12.4	12.4	12.4	12.4	12.2	12.0	11.8	11.8
151	151	150.5	147.5	146.5	145.5	145.5	144.5	144.5	142.5	140.5	138.5	137.5
30	32 33	35	36	37	38	39	40	41	42	43	44	45

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Objectives: Caenorhabditis elegans
C. Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C. Accession: T27179
C. Rallis, J.
S. Wallis, J.
S. Wallis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPRVVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 LDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNGCPEF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
hypothetical protein Y54G11A.10 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.6%; Score 662; DB 2; Le 68.4%; Pred. No. 2.5e-42; Live 30; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 68.45
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 IRSTQOSPIL 306
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hypothetical protein C25F6.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999 C;Accession: T15617 R;BentLey, D. submitted to the EMBL Data Library, October 1995 A;Bescription: The sequence of C. elegans cosmid C25F6. A;Reference number: Z18377 A;Accession: T15617 A;Status: preliminary; translated from GB/EMBL/DDBJ

2

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discs-large tumor suppressor - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A33651
R; Woods, D.F.; Bryant, P.J.
Cell 66, 451-464, 1991
A; Title: The discs-large tumor suppressor gene of Drosophila encodes a guanylate kin. A; Reference number: A39651; MUID:91330294; PMID:1651169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase C;Keywords: signal transduction F;45-123/Domain: GLGF domain homology <GLG1>
                                                                        GLGF domain homology; guanylate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-960 < MOO>
A; Residues: 1-960 < MOO>
A; Cross-references: 68:M73529; NID:q157243; PIDN:AAA28468.1; PID:q157244
C; Comment: Loss of this protein causes large imaginal disks by allowing neoplastic cition to control cellular proliferation.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ϊ;
                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 HSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --EPRKVVLHKGSTGLGFNIVGG-EDGEGIFVSFILAGGPADLSGELQRGDQILSVNGID 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | ||:| || || :| :: :| |: || || 475 LRGASHEQAAAALKGAGGTVTIIAQYQPEDYARFEAKIHDLREQWMNHSMSSGSGSLRTN 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 ATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synapse-associated protein SAP90 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 GEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNGCPEFRARATAKATVAAFAASEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 GLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEMEARFEKLR 204
                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                          Length 870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 960;
                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 VEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR--
                                                                                                                                                                                                                                                                                                                                                                                                 GLLPDSEMTS----HSQHSTATRQPSMTLQRAVSLEG---
                                                                                                                                                                                                                                                ,7e-08;
les 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%; Score 208.5; DB 139.3%; Pred. No. 8.9e-08;
                                                            C.Superfamily: discs-large tumor suppressor; GLGF F;198-276/Domain: GLGF domain homology <GLG2> F;543-601/Domain: SH3 homology <SH3> F;681-858/Domain: guanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;159-241/Domain: GLGF domain homology <GLG2>
F;491-563/Domain: GLGF domain homology <GLG3>
F;607-665/Domain: SH3 homology <SH3-
F;771-948/Domain: guanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                  31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Mismatches
                                                                                                                                                                                                                      Score 217.5;
Pred. No. 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: FlyBase:dlg1
A;Cross-references: FlyBase:FBgn0001624
                                                                                                                                                                                                                      Query Match 18.6%;
Best Local Similarity 29.3%;
Matches 55; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKRSLYVR 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 QQQQLLIQ 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                    385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Incitation: Cloning of new isoforms of PSD-95/SAP90 related genes.
A; Reference number: 217166
A; Reference number: 217166
A; Reference number: 217166
A; Reference number: 217166
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: Instance: EMBL:U53368; NID:g1517939; PID:g1517940
A; Residues: Instance: EMBL:U53368; NID:g1517939; PID:g1517940
C; Genetics:
A; Note: PSD-95/SAP90-related gene 2 (chapsyn isoform2)
C; Superfamily: discs-large tumor suppressor; GLGF domain homology <GLGC
C; Superfamily: discs-large tumor suppressor; GLGF domain homology <GLGC
C; Superfamily: discs-large tumor suppressor; GLGF domain suppressor; F; 543-601/Domain: SH3 homology <GRI>F; 663-840/Domain: GLGF domain suppressor; F; 663-840/Domain: GLGF domain suppressor; GLGF domain suppressor; F; 663-840/Domain: SH3 homology <GRI>F; 663-840/Domain: GLGF domain suppressor; GLGF domain suppressor; F; 663-840/Domain: SH3 homology <GRI>F; 663-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homo
                                                     A;Cross-references: EMBL:U39742; NID:g1049455; PID:g1049459; PIDN:AAA80434.1; CESP:C25F'C;Genetics:
A;Genetics: A;Gene: CESP:C25F6.2
A;Gene: CESP:C25F6.2
A;Introns: 105/1; 210/3; 283/3; 316/1; 346/2; 463/3; 566/1; 722/2; 897/1; 991/2; 1032/1
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                                                                                                                                                                                                                                                                                                                                     106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                                        147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 ATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHG
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                Length 1131;
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                                                                                                                                                                                                                                                                            Indels
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A; Residues: 1-870 <KIM>
A; Cross-references: EMBL: U32376; NID: 91463025; PID: 91036790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                       20.0%; Score 233.5; DB 2; '0.5%; Pred. No. 1.5e-09; '0.5%; Pred. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.7%; Score 219; DB 2; L. 35.7%; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, July 1995
A; Reference number: G08966
AAccession: G01974
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                                                                                                                                                                                                                                                                            Conservative
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                                  1-1131 <BEN>
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Best Local Simi
Matches 51;
A; Molecule type:
                                                                                                                                                                                                                                                                         48;
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                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                Best Local
Matches 4
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homologue of the Drosophila
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C:Species: Homo saptems charge process;

C:Species: Homo saptems (man)

C:Species: Homo saptems (man)

C:Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000

R:Lude, R.A.: Marfata, S.M.; Branton, D.; Chishti, A.H.

Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994

A;Fitle: Cloning and characterization of hdlg: the human homologue of the Drosop A; Reference number: 138756; MUD:95024052; PMID:7937897

A; Reference number: 138756; MUD:95024052; PMID:7937897

A; Residues: 1-904 < RES>

A; Residues: 1-904 < RES>

A; Cross-references: EMBL:013897; NID:9558437; PIDN:AAA50599.1; PID:9558438

A; Cross-references: GDB:393278; OMIM:601014

A; Cross-re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 767;
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                                                                                                                                                                                                                       NID: 93318652; PID: 93318653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                               A.Status: preliminary; translated from GB/EMBL/DDBJ A.Status: preliminary; translated from GB/EMBL/DDBJ A.Status: preliminary; translated from GB/EMBL/DDBJ A.Status: preliminary
A.Status: 1-767 CSTA>
A.Cross-references: EMBL:U83192; NID:g3318652; PID:g33:
A.Status: BABL:U83192; NID:g3318652; PID:g33:
A.Status: BABL:U83192; NID:g3318652; PID:g33:
A.Gene: PSD95
C.Superfamily: discs-large tumor suppressor; GLGF doma:
F.208-286/Domain: GLGF domain homology <GLG>
F.478-586/Domain: GlGF domain homology <GKI>
F.578-755/Domain: guanylate kinase homology <GKI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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16.4%; Score 192; DB 2;
Best Local Similarity 35.2%; Pred. No. 1.4e-06;
Matches 44; Conservative 23; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.8%; Score 196.5; DB 3
Best Local Similarity 41.4%; Pred. No. 5.4e-07;
Matches 41; Conservative 19; Mismatches 38
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                         A; Reference number: Z16761
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C;Accession: A45436
R;Kistner, U.; Wenzel, B.M.; Veh, R.W.; Cases-Langhoff, C.; Garner, A.M.; Appeltauer, U.
J. Biol. Chem. 268, 4580-4583, 1993
A;Title: SAP90, a rat presynaptic protein related to the product of the Drosophila tumor A;Reference number: A45436
A;Title: SAP90, a rat presynaptic protein related to the product of the Drosophila tumor A;Reference number: A45436
A;Accession: A45436
A;Accessi
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N*Alternate names: brain specific PSD-95 protein; discs-large tumor suppressor protein h
N*Alternate names: brain specific PSD-95 protein; discs-large tumor suppressor protein h
N*Alternate names: brain specific PSD-95 protein; discs-large tumor suppressor protein h
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
N*Cho, K.O.; Hunt, C.A.; Kennedy, M.B.
Neuron 9, 929-942, 1992
Neuron 9, 929-942, 1992
A;Title: The rat brain postsynaptic density fraction contains a homolog of the drosophil A;Reference number: JH0800; MUID:93040233; PMID:1419001
A;Accession: JH0800.
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C.Species: Homo sapiens (man)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C.Accession: T09599
R.Stathakis, D.G.; Hoover, K.H.; You, Z.; Bryant, P.J.
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A,Residues: 1-724 <CHO>
A,Cross-references: GB:M96853; NID:g206454; PIDN:AAA41971.1; PID:g206455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 196.5; DB Pred. No. 5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Mismatches
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Best Local Similarity
Matches 41; Conserv
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OY 213 QLLIQ 217   ::   583 SLYVR 587	RESULT 12 T30259 multiple PDZ domain protein - mouse C:Species: Mus musculus (house mouse) C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000	C;Accession: 130259 R;Simpson, E.H.; Suffolk, R.; Jackson, I.J. R;Simpson, E.H.; Suffolk, R.; Jackson, I.J. Genomics 59, 102-104, 1999 A;Title: Identification, sequence, and mapping of mouse multiple PDZ domain protein A;Reference number: 220797; MUID:99326529; PMID:10395806 A;Accession: T30259 A;Status: preliminary: translated from GB/FMBL/DDBJ	A; Molecule type: mRNA A; Residues: 1-2055 <sim> A; Cross-references: EMBJ: AJ131869; NID: 94150877; PIDN: CAA10523.1; PID: 94150878 A; Experimental source: strain C57/BL6 X CBA F1; whole brain C; Genetics: A; Gene: mpdz</sim>	A;Map position: 4 Query Match Best Local Similarity 29.0%; Pred. No. 4.2e.06; Matches 56; Conservative 31; Mismatches 81; Indels 25; Gaps 4;	OY 1 MLKPSVTSAPTADNATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKV 56	OY 57 LOSEFCTAIREVYQYMHETITVNGCPEFRARATVAAFAASEGHSHPRVVELPKTDE 116	QY 117 GLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSGEHHBKAVE 173          ::   :   :	Qy 174 LLKAAKDSVKLVV 186 :    :   :  Db 2041 ILKRTKGTVTLMV 2053	RESULT 13 T46612 multi PD2 domain protein 1 - rat C, Species: Rattus norvegicus (Norway rat) C; Species: Rettus norvegicus (Norway rat) C; Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text change 21-Jul-2000	C; Accession: T46612 R; Ullmer, C.; Schmuck, K.; Figge, A.; Lubbert, H. FEBS Lett. 424, 63-68, 1998 A; Title: Cloning and characterization of MUPP1, a novel PDZ domain protein. A; Reference number: 223104; MUID: 98196865; PMID: 9537316 A; Accession: T46612 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molenie Type: mRNA A; Residues: 1-2054 curi.>	A;Cross-references: EMBL:AJ001320; NID:g2959978; PIDN:CAA04681.1; PID:g2959979 A;Experimental source: brain C;Genetics: A;Gene: MUPP1	Query Match Best Local Similarity 28.5%; Pred. No. 9.9e-06; Matches 55; Conservative 31; Mismatches 82; Indels 25; Gaps 4;	QY 1 MLKPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKV 56  :  :    :     :     :
C; Species: Rattus norvegicus (Norway rat) C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000 C; Accession: 156552 R; Muller, B.M.; Kistner, U.; Veh, R.W.; Cases-Langhoff, C.; Becker, B.; Gundelfinger, E.J., Neurosci. 15, 2354-2366, 1995	al distribution of SAP97, a novel presynapt ID:7891172 L/DDBJ	; PID:g642456 ology; guanylate Kinase homc	2; Length 911; 06; 44; Indels 14; Gaps 2; GVAERHGGLKRGDQLLSVNGVSVBG 165	Db 463 PRKVVLHRGSTGLGFNIVGG-EDGEGIFISPILAGGPADLSGELRKGDRIISVNSVDLRA 521  Qy 166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKIRTARRRQQQ 212	213 QLLIQ 217   1:1 582 SIVR 586	SULT 11 8756	homolog of Drosophila discs large protein, isoform 2 - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Profession 12875	C, ACCESSION: 130/30  K; Lue, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.  Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994  A; Title: Cloning and characterization of hdlg: the human homologue of the Drosophila dis  A; Reference number: 138756; MUID:95024052; PMID:7937897	A. Accession: 130.730 A. Molecule type: mRNA A. Mesidues: 1-926 < RES> A. Cross references: EMBL:U13896; NID:9558435; PIDN:AAA50598.1; PID:9558436 C. Genetics:	A; Gene: GDB:DLG1 A; Caross-references: GDB:393278; OMIM:601014 A; Cross-references: GDB:393278; OMIM:601014 A; Map position: 3429-3428 C; Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase homc C; Keywords: alternative splicing; duplication F; 229-307/Domain: GLGF domain homology <glg2> F; 524-402/Domain: GLGF domain homology <glg2> F; 534-402/Domain: SH3 homology <sh3> F; 537-914/Domain: GLGF domain homology <grc3> F; 540-402/Domain: GLGF domain homology <grc3></grc3></grc3></grc3></grc3></grc3></sh3></glg2></glg2>	Ouery Match 16.4%; Score 192; DB 2; Length 926; Best Local Similarity 35.2%; Pred. No. 1.5e-06; Matches 44; Conservative 23; Mismatches 44; Indels 14; Gaps 2;	QY 106 PRVVELPKIDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165	Qy 166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLRTARRRQQQ 212   :

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Search completed: September 23, 2003, 15:15:21 Job time: 20 secs
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A.Molecule type: DNA
A.Residues: 1-431 <BEN>
A.Residues: 1-431 <BEN>
A.Cross-references: EMBL:U49829; NID:g1203924; PID:g1203931; PIDN:AAA93388.1; CESP:F27D9
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A;Introns: 8/1; 52/3; 74/1; 96/1; 128/2; 149/3; 199/2; 255/3; 297/3; 319/3; 350/3; 390/3
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                                                                                     ---HQQELANPCLAF----TGLTSSTIFPDDLGPPQSKTITLDRGPD 1979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted to the EMBL Data Library, January 1996
A; Reference number: 219701
A; Recession: 123160
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1012 < WILL>
A; Cross-references: EMBL: 268750; PIDN: CAA92965.1; GSPDB: GN00022; CESP: K01A6.1
A; Experimental source: clone K01A6
C; Genetics: Constitution of the constitution 
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: D-Sep-1999 #sequence_revision 20.Sep-1999 #text_change 20.Sep-1999
C;Accession: T16191
R;BentLey, D.
Submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid F27D9.
A;Reference number: Z18473
A;Accession: T16191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein KOlA6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C;Accession: T23160
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A:Introns: 107/1: 151/2: 183/2: 270/2: 316/3: 410/3: 628/3: 922/3: C:Superfamily: WW repeat homology
F:131-168/Domain: WW repeat homology < WWR>
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Pred. No. 9.3e-06;
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34.4%;
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                             107 RVVELPKTDEGLGFNVMGGKE--QNSPIYISRIIPGGVABRHGGLKRGDQLLSVNGVSVE 164
                                                                                      165 GEHHEKAVELLKAAKDSVKLVVRY----TP----KVLE---EMEARFEKLRTARRRQQQ 212
                                                                                                       95
                                            Gaps
 14;
 46; Indels
 26; Mismatches
 45; Conservative
                                                                                                                                                                    156 ESRLSDSKWQQ 166
                                                                                                                                             213 QLLIQQQQQQQ 223
 Matches
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version 5.1.6
- 2003 Compugen Ltd.
  GenCore
Copyright (c) 1993
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using sw model protein search, OM protein -

September 23, 2003, 15:11:13; Search time 12 Seconds (without alignments) 913.102 Million cell updates/sec Run on:

us-09-909-005-1 Title: Perfect score:

1 MLKPSVTSAPTADMATLTVV.....LLIQQQQQQQQQQQQTQQNHMS 233 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NEB1_HUMAN LNX2_MOUSE	NEBI_RAT PTP1_CAEEL SHK3_RAT	PA3L_HUMAN LNX2_HUMAN STG1_HUMAN	STG1_MOUSE PTN4_HUMAN MPP6_MOUSE PCLO_MOUSE
ММ	~ ~ ~		
742	1095 1026 1815	1205 690 517	517 926 553 5038
12.3	12.0 11.8 11.8	11.7	11.2 11.0 11.0 10.8
143.5	140.5 137.5 137.5	137 136.5 134	130.5 129 126.5
33.5	38 38 38	39 40 41	4444 1045

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegious (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-96193770; PubMed=8625413;

MEDLINE-96193770; PubMed=8625413;

MEDLINE-96193770; PubMed=8625413;

Santillano D.R., Wu Z., Huang F., Xia H., Peters M.F.,

Froehner S.C., Bredt D.S.;

Froehner S.C., Bredt D.S.;

Protein PSD-95 and alphal-syntrophin mediated by PDZ domains.";

Cell 84:757-767(1996).
                             063622; P70548; Q62939; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Channel associated protein of synapse-110 (Chapsyn-110) (Synaptic density protein PSD-93) (Discs, large homolog 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96310881; PubMed-8755482;
Kim E., Cho K.O., Rothschild A., Sheng M.;
"Heteromultimerization and NMDA receptor-clustering activity
Chapsyn-110, a member of the PSD-95 family of proteins.";
Neuron 17:103-113(1996).
   852 AA.
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EMBL; U50717, AAC52643.1; -.
EMBL; U53368; AAB48562.1; -.
PIR; T10811; T10811.
HSSP; Q12959; IPDR.
InterPro; IPRO00619; Guanylate_kin.
InterPro; IPRO01478; PDZ.
PRT;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
DLG2_RAT
   HERE THE PROPERTY OF THE PROPE
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SEQUENCE FROM N.A.

MEDLINE=96310881; PubMed=8755482;

Kim E., Cho K.-O., RothSchild A., Sheng M.;

Heteromultimerization and NWDA receptor-clustering activity of Chapsyn-110, a member of the PSD-95 family of proteins.";

Neuron 17:103-113(1996).

-! FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPTOR SUBUNITS AS WELL AS POTASSIUM CHANNELS.
-! SINILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
-! SIMILARITY: Contains 3 PG2-DHR domains.
-! SIMILARITY: Contains 1 PH3. domain.
-! SIMILARITY: Contains 1 guanylate kinase-like domain.
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GUANYLATE KINASE.
89C83BA0619F6F59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ## WELLY | BONC.12911; DIG2.
## GO1 GO:0005886; C:plasma membrane; TAS.
## GO2 GO:0005886; C:plasma membrane; TAS.
## GO3 GO:0004385; F:guanylate kinase activity; TAS.
## InterPro; IPR001478; PDZ.
## InterPro; IPR001478; PDZ.
## InterPro; IPR001478; PDZ.
## InterPro; IPR001478; PDZ.
## PFAM: PF00625; Guanylate_kin; 1.
## PFAM: PF00625; Guanylate_kin; 1.
## PFAM: PF00625; PDZ; 3.
## PFAM: SM0072; GukC; 1.
## SMART; SM00726; GukC; 1.
## SMART; SM00726; GukC; 1.
## SMART; SM00726; GukC; 1.
## PROSITE; PS00866; GUANYLATE_KINASE_1; 1.
## PROSITE; PS00002; SH3; 1.
## PROSITE; PS50002; SH3; 1.
## PROSITE; PS50002; SH3; 1.
## PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%; Score 217.5; DB 1; 29.3%; Pred. No. 1.8e-08; Live 31; Mismatches 59;
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PDZ 2.
PDZ 3.
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HSSP; Q12959; 1PDR.
Genew; HGNC:2901; DLG2.
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279
501
606
870
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Best Local Similarity
Matches 55; Conserv
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015700.
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Channel associated protein of synapse-110 (Chapsyn-110) (Discs, large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 ATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 ATRQPSVTLQRAISLEGEPRKVVLHKGSTGLGFNIVGG-EDGEGIFVSFILAGGPADLSG
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.7%; Score 219; DB 1; Length 852; 35.7%; Pred. No. 1.4e-08; Live 24; Mismatches 54; Indels
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B -> E (IN REF. 2)

D -> E (IN REF. 2)

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D -> H (IN REF. 2)

D -> H (IN REF. 2)

R -> P (IN REF. 2)

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C -> Q (IN REF. 2)
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F -> L (IN REF. 1).
N -> Y (IN REF. 2).
E -> V (IN REF. 1).
L -> H (IN REF. 2).
KR -> NG (IN REF. 2).
T -> M (IN REF. 2).
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VR -> IL (IN REF.
                         Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00655; PDZ; 3.
Pram; PF00018; SH3; 1.
Probom; PD000066; SH3; 1.
SMART; SM00072; GuKc; 1.
SMART; SM00126; PDZ; 3.
SMART; SM00326; PDZ; 3.
PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50106; PDZ; 3.
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nes 51; Conservative
InterPro; IPR001452; SH3
                                                                                                                                                                                                                                                                                                                             SH3 domain, Repeat.

DOMAIN

DOMAIN

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CONFLICT

CONFLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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m

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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara O.;
                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLG3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
       DARADO DARA RELEGIA DE LA RESERVA DO LA RESERVA DO LA RESERVA DE LA RESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseefisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO: 00.0045179; C:apical cortex; IDA.
GO: 00.0015327; C:apical cortex; IDA.
GO: 00.0005918; C:apical cortex; IDA.
GO: 00.0005918; C:apical cortex; IDA.
GO: 00.0005918; C:apical plasma membrane; IDA.
GO: 00.0007391; P:basal protein localization; IMP.
GO: 00.0007391; P:catallishment and/or maintenance of epithel. .; NAS.
GO: 00.0016334; P:establishment and/or maintenance of polarit. .; IGI.
GO: 00.0016336; P:establishment and/or maintenance of polarit. .; NAS.
GO: 00.0007399; P:regulation of synapse; IMP.
InterPro: IPR000619; Guanylate_kin.
InterPro: IPR001478; PDZ.
InterPro: IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reproductive tissues.
-!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically throughout development.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
-!- SIMILARITY: Contains 3 PDZ/DHR domains.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Plays a critical role at septate junctions in cellular growth control during larval development. The presence of a guantylate kinase domain suggests involvement in cellular adhesion as well as signal transduction to control cellular proliferation. Required for maintenance of cell polarity.
-!- SUBCELLULAR LOCATION: CYTOSKELETON-ASSOCIATED. LOCATED AT THE CYTOPLASMIC FACE OF THE MEMBRANE IN THE CELLULAR BLASTODERM AND BECOMES ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM BETWEEN EPITHELIAL CELLS AT THE TIME OF DORSAL CLOSURE. IN ADULT FLIES, LOCATED AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: In embryos, expression is seen in epithelial cells and some nervous tissue. In larvae, expression is seen as a belt around salivary glands and imaginal disks, also in proventriculus and parts of the brain. Expressed in adult
                                                                                                                                                                                                                                                                                                                                                                                                                        "The discs large tumor suppressor gene of Drosophila encodes a guanylate kinase homolog localized at septate junctions."; Cell 66:451-464(1991).
                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpĥa;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=1;
Comment-A number of isoforms are produced;
                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P31007-1; Sequence=Displayed;
                                                                                                                            tumor suppressor protein.
                                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=91330294; Pubmed=1651169;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M73529; AAA28468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0001624; dlg1.
                                                                                                                                                                                                                                                                                                                                                                                                      Woods D.F., Bryant P.J.;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPITHELIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A39651; A39651
HSSP; P31016; 1BFE.
                                                                                                                                                   DLG1 OR L(1) DLG1
                                                                                                                            Discs large-1
DLG1_DROME
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88 ATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHG 147
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DNA Res. 6:37-345(1999).
-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR SUBGNUT NR2B (BY SIMILABRILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 AVPPGTPRAVSTEDITREPRITITIQKGPQGLGFNIVGG-EDGQGIYVSFILAGGPADLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 GLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Makino K., Kuwahara H., Masuko N., Nishiyama Y., Morisaki T., Sasaki J., Nakao M., Kuwano A., Nakata M., Ushio Y., Saya H.; "Cloning and characterization of NE-dlg: a novel human homolog of the Drosophila discs large (dlg) tumor suppressor protein interacts with the APC protein."; Oncogene 14:2425-2433(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
-:- SIMILARITY: Contains 3 PDZ/DHR domains.
-:- SIMILARITY: Contains 1 SH3 domain.
-:- SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIGGLHUMAN STANDARD; PRT; 817 AA.
092796; Q9UL18;
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Presynaptic protein SAPI02 (Synapse-associated protein 102)
(Neuroendocrine-DLG) (NE-DLG) (Discs, large homolog 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102468 MW; BF87A4262F1B6AD5 CRC64;
                                                                            Prodom, PD000066; SH3; 1.
SMART; SM00028; PD2; 3.
SMART; SM00028; PD2; 3.
SMART; SM00028; PD2; 3.
PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50106; PD2; 3.
PROSITE; PS50100; PD2; 3.
PROSITE; PS50002; SH3; 1.
Transducer; SH3 domain; Alternative splicing; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 208.5; DB 1;
Pred. No. 9.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
                                                                                                                                                                                                                                                                                                                                              PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=20039619; PubMed=10574462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal brain;
MEDLINE=97332623; PubMed=9188857;
PF00625; Guanylate_kin; 1.
PF00595; PDZ; 3.
PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 330-817 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Conservative
                                                                                                                                                                                                                                                                                                                                                                        154
486.
600
768
960 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLG3 OR KIAA1232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDZ 1.
PDZ 3.
PDZ 3.
SU3.
GUANYLATE KINASE.
FTALADNHISHNSSLGYLGAVESKVSYPAPPQVPPTRYSPI
PRHMLAEEDFT -> AARRERGAMERRARKFSGSGLAMGLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFPGLSDDYYGAKNI -> SIKTKRKKSFRLSRKFPFYKSK
ENMAQESSLOEQGYTSNTSDSESSS (IN REF. 2).
3D7512EC4713FC4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Presynaptic protein SAP102 (Synapse-associated protein 102) (Discs, large homolog 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASASAWRRASQRWAWPLRSLRPGGDA (IN REF. 2)
                                                                                                                EMBL; U49089; AAB61453.1; -.

EMBL; AB033058; BAA86546.1; -.

EMSP; Q12959; IPDR.

Genew; HGNN:2902; DLG3.

MIM; 300189; -.

GO; GO:00004385; F:guanylate kinase activity; NAS.

GO; GO:00008285; P:negative regulation of cell proliferation; NAS.

InterPro; IPR001619; Guanylate_Kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.4%; Score 203.5; DB 1; Length 817; 43.4%; Pred. No. 1.8e-07; tive 18; Mismatches 37; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 ATHEQAAAALKRAGQSVTIVAQYRPEEYSRFESKIHDLR 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            849 AA
                                                                                                                                                                                                                                               InterPro; IPR001452, SH3.
Pfam; PF00625; Guanylate_Kin; 1.
Pfam; PF006155; PD2; 3.
Pfam; PF00018; SH3; 1.
ProDom; PF000066; SH3; 1.
SMART; SM00722 (UKC; 1.
SMART; SM00226; PD2; 3.
SMART; SM00226; SH3; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50062; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                          \vec{-}
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STRAIN-C57BL/6; TISSUE-Brain;
Kohmura N., Makino S., Yagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   817 AA; 90344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       909
                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLG3 OR DLGH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLG3_MOUSE
P70175;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
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DOMAIN
DOMAIN
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DLG3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                           -:- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
-:- SIMILARITY: Contains 3 PDZ/DHR domains.
-:- SIMILARITY: Contains 1 SH3 domain.
-:- SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLG3_RAT STANDARD; PRT; 849 AA.
DLG3_RAT STANDARD;
DLG180; P70547;
DLNOV-1997 (Rel. 35, Created)
101-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Presynaptic protein SAP102 (Synapse-associated protein 102) (PSD-DLG3.
DLG3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Brain;
MEDLINE-96374358; PubMed-8780649;
Mueller B.M., Kistner U., Kindler S., Chung W.J., Kuhlendahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUANYLATE KINASE.
EF3EF2D7513538EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 ATHEQAAALKRAGOSVIIVAQYRPEEYSRFESKIHDLR 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.4%; Score 203.5;
                                                                                                                                                                                                                                                                   MGD: MGI:1888986; D19h3.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
Probom; PP000186; SH3; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00228; PDZ; 3.
SMART; SM00228; PDZ; 3.
PROSITE; PS500165; SH3; 1.
PROSITE; PS500165; GUANYLATE_KINASE_1; 1.
PROSITE; PS500165; DPZ; 3.
PROSITE; PS500165; PDZ; 3.
PROSITE; PS500165; DPZ; 3.
PROSITE; PS500165; PDZ; 3.
PROSITE; PS500165; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  \vdots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDZ 1.
PDZ 2.
PDZ 3.
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM LONG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93482 MW;
                                                                                                                                                                                                                                             EMBL; D87117; BAA13249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484
589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404
519
659
849 AA;
                                                                                                                                                                                                                                                             ; 1PDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                SUBUNIT NR2B
                                                                                                                                                                                                                                                             HSSP; Q12959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLG3_RAT
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Presynaptic density protein 95 (PSD-95) (Presynaptic protein SAP90)
CSynapse-associated protein 90) (Discs, large homolog 4).
DLG4 OR DLGH4 OR PSD95.
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-DBA/2; TISSUE-Brain;
                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
      SO THE THE TRANSPORT THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 PRKIILHKGSTGLGFNIVGG-EDGEGIFVSFILAGGPADLSGELRRGDRILSVNGVNLRN 460
                                                                                                                                                                                                                   Irle M., Hata Y., Takai Y.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NWDA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISO 26-26-29. Sequence-VSP_003151;
--- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
--- SIMILARITY: Contains 3 PDZ/DHR domains.
--- SIMILARITY: Contains 1 SH3 domain.
--- SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Fenster S.D., Lau L.-F., Veh R.W., Huganir R.L., Gundelfinger E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>,</del>
                          Garner C.C.; "SAP102, a novel postsynaptic protein that interacts with NMDA receptor complexes in vivo."; Neuron 17:255-265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GUANTLATE KINASE.
Missing (in isoform Short).
/FTId=VSP_003151.
34DA9C46C7BB96DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 ATHEQAAAALKRAGQSVIIVAQYRPEEYSRFESKIHDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR
                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.4%; Score 203.5; DB 1
43.4%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U50147; AAA93031.1; --
EMBL; U53367; AAA48561.1; --
HSSP; O12959; IDDR.
InterPro; IPR001619; Guanylate_kin.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00619; PDZ.
Pfam; PF00619; SH3.
I.
ProDom; PD00018; SH3; 1.
ProDom; P000108; SH3; 1.
ProDom; SM0072; GuKc; 1.
SWART; SM00228; PDZ, 3.
SWART; SM00326; SH3; 1.
PROSITE; PS50052; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50062; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=062936-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing.
235 PDZ 1.
330 PDZ 2.
184 PDZ 3.
                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93539 MW;
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                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat;
149 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                  SUBUNIT NR2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                             Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH3 domain;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   datches
RRYRY RYRY RRYRY R
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106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.8%; Score 196.5; DB 1; Length 724; 41.4%; Pred. No. 4.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7EFFC99E1FFF90BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SH3.
GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piam; PF00625; Guanylate_kin; 1.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF0018; SH3; 1.
Probom; PD00066; SH3; 1.
SMART; SM000228; PD2; 3.
SMART; SM00328; PD2; 3.
SMART; SM00326; SH3; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 3.
PROSITE; PS50106; PD2; 3.
PROSITE; PS50106; PD2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1277959; Dlgh4.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D50621; BAA09297.1; -. HSSP; P31016; 1BE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 724 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3 domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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724 A.

PRT;

STANDARD;

DLG4\_MOUSE

DLG4\_MOUSE

RESULT 7

9

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modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00856; GUANYLATE_KINASE_1; 1. PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                   Guanylate_kin.
                                                                                                                                                                                               PDB; 1BEB; 21-CCT 98.

PDB; 1BFE; 21-CCT 98.

PDB; 1JXUM; 16-JAN-02.

PDB; 1JXUW; 01-MAY-02.

PDB; 1QCC; 06-FEB-00.

InterPro; 1PR001478; PDZ.

InterPro; 1PR001478; PDZ.

InterPro; 1PR001478; PDZ.

Ffam; PP00525; PDZ; 3.

Pfam; PP000625; Quanylate_kin; 1.

Pfam; PP000625; Quanylate_kin; 1.

Pfam; PP00018; SH3; 1.

SMART; SM00228; PDZ; 3.

SMART; SM00228; PDZ; 3.

SMART; SM00228; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D-structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80465 MW;
                                                                                                  EMBL; M96853; AAA41971.1; -.
EMBL; X66474; CAA47103.1; -.
EMBL; U77090; AAB38270.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
393
498
724
61
78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat;
                                                                                                                                                                               JH0800; JH0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                724 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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160
3313
428
534
61
78
177
200
254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
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CONFLICT
CONFLICT
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          COCCO COCOCO COCCO COCCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH DLGAP1 AND SHANK PROTEINS.
MEDLINE=9945865; PubMed=10527873;
MEDLINE=9945865; PubMed=10527873;
MEDLINE=9745865; PubMed=10527873;
Seidenbecher C., Garner C.C., Gundelfinger E.D.;
"Proline-rich synapse-associated proteins ProSAP1 and ProSAP2 interact with synaptic proteins of the SAPAP/GAPF family,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).

-!-SUBCELDIANE LOCATION: Cytoplasmic. Concentrated at synaptic junctions primarily on the presynaptic side. Also found in postsynaptic density of neuronal cells.
-!-TISSUE SPECIFICITY: PRESYNAPTIC DENSITY FRACTION OF BRAIN.
-!-SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
-!-SIMILARITY: Contains 3 PDZ/DHR domains.
-!-SIMILARITY: Contains 1 SH3 domain.
-!-SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                           Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_raxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96270509; PubMed=8674113; Doyle D.A., Lee A., Charks J., Kim E., Sheng M., Mackinnon R.; Doyle D.A., Lee A., Charks J., Kim E., Sheng M., Mackinnon R.; Crystal structures of a complexed and peptide-free membrane protein-binding domain: molecular basis of peptide recognition by PDZ."; Call 85:1067-1076(1996).

-! FUNCTION: Interacts with the cytoplasmic tail of NMDA receptor subunits. May be involved in synaptogenesis.

-! STRUNIT: Interacts with DIGARPI/GRAP. Is part of a complex with DIGARPI/GRAP. STRUMY: Interacts with DIGARPI/GRAP. Is part of a complex with DIGARPI/GRAP, SHANK! SHANK2 or SHANK3. Interacts through its third PDG Gomain with NLGNI, and probably with NLGN2 and NLGN3 (By
                                                                                                                      DIG4_RAT
P31016; P97631;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Presynaptic density protein 95 (PSD-95) (Presynaptic protein SAP90)
(Synapse-associated protein 90) (Discs, large homolog 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cho K.-O., Hunt C.A., Kennedy M.B.; "The rat brain postsynaptic density fraction contains a homolog of the Drosophila discs-large tumor suppressor protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garner A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SERAMIN=Spraque-Dawley; IISSUE-Brain;
MEDLINE=93186719; Pubmed=7680343;
Kistner U., Wenzel B.M., Veh R.W., Cases-Langhoff C., Garner A.M.
Appeltauer U., Voss B., Gundelfinger E.D., Garner C.C.;
"SAP90, a rat presynaptic protein related to the product of the Drosophila tumor suppressor gene dig-A.";
J. Biol. Chem. 268:4580-4583(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle; Adams L.D., Werny I., Schwartz S.M.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.82 ANGSTROMS) OF 302-402
370 ASHEQAAIALKNAGQTVTIIAQYKPEEYSRFEAKIHDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 264:247-252(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley, TISSUE=Brain;
MEDLINE-93040233; PubMed=1419001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 566-625 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuron 9:929-942(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                          RESULT 8
                                                                                                    DLG4_RAT
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entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> SLDPPKTVPTMIFSPSS (IN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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P78352, 092941; O9UKK8;
01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Presynaptic density protein 95 (PSD-95) (Discs, large homolog Postsynaptic density -95).
DLG4 OR PSD95.
HOMO Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M -> L (IN REF. 2).
S -> T (IN REF. 2).
GVGNCH -> ALGTSI (IN REF. 2).
A -> G (IN REF. 2).
S -> T (IN REF. 2).
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Usage by
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GKH -> RDQ (IN REF. 3).
7922D4E8E0F9AD85 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.8%; Score 196.5;
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SEQUENCE FROM N.A.
TISSUE=Mammary gland;
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41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c. 1. FUNCTION: Interacts, with the cytoplasmic tail of NWDA receptor subunits. May be involved in synaptogenesis.

c. 1. SUBUNIT: Interacts with DIGAPI/GKAP (BPS similarity). Is part of a complex with DIGAPI/GKAP (BPS similarity). Is part of a complex with DIGAPI/GKAP. SHANKI OF SHANK3 (By similarity). Binds to KIFIJB. Interacts through its third PDZ domain with NIGNI. and probably with NIGNZ and NIGNS.

c. 1. SUBCELLULAR LOCATION: Cytoplasmic. Concentrated at synaptic junctions primarily on the presynaptic side. Also found in postsynaptic density of neuronal cells (By similarity).

c. 1. SIMILARITY: Contains 3 PDZ/DHR domains.

c. 1. SIMILARITY: Contains 1 SH3 domain.

c. 1. SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brenman J.E., Bredt D.S., Parkinson J.F., Manzana W.P., McClary J.A.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDIAGE=10582582;
MEDLINE=20047407; PubMed=10582582;
Stathakis D.G., Udar N., Sandgren O., Andreasson S., Bryant P.J.,
Small K., Forsman-Semb K.;
"Genomic organization of human DLG4, the gene encoding postsynaptic
                             Stathakis D.G., Hoover K.B., You Z., Bryant P.J.;
"Human postsynaptic density-95 (PSD95): location of the gene (DLG4) and possible function in nonneural as well as in neural tissues.";
Genomics 44:71-82(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Irie M., Hata Y., Takeuchi M., Ichtchenko K., Toyoda A., Hirao K.
Takai Y., Rosahi T.W., Suedhof T.C.;
"Binding of neuroligins to PSD-95.";
Science 277:1511-1515(1997).
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R InterPro; IPR001478; PDZ. R InterPro; IPR001478; PDZ. R PPEMD; PPEMD;
                                                                                                                                                                                                                                               Stathakis D.G., Hoover K.H., You Z., Bryant P.J.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH NLGN1; NLGN2 AND NLGN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurochem. 73:2250-2265(1999).
MEDLINE=97432822; PubMed=9286702;
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EMBL; AF156495; AAD56173.1; -.
EMBL; U68138; AAB07736.1; -.
PIR; T09599; T09599.
PDB; IKEF; 06-MAR-02.
Genew; HGNC:2903; DLG4.
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                                                                                                                                                                                                                     IISSUE=Mammary gland;
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MIM; 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE MACKY FAMILY OF CELL JUNCTION PROTEINS.
-!- SIMILARITY: Contains 1 SH3 domains.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 guanylate kinase-like domain.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-95024052; PubMed-7937897;
Lue R.A., Marfatia S.M., Branton D., Chishti A.H.;
"Clohing and characterization of hdig: the human homologue of th
Drosophila discs large tumor suppressor binds to protein 4.1.";
Proc. Natl. Acad. SCI. U.S.A. 91:9818-9822(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             16.8%; Score 196.5; DB 1; Length 767; 41.4%; Pred. No. 5.3e-07;
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MEDLINE-96338231; PubMed-8757139;
Cabral J.H., Petosa C., Sutcliffe M.J., Raza S., Byron (Marfatia S.M., Chishti A.H., Liddington R.C.;
"Crystal structure of a PDZ domain.";
Nature 382:649-652(1996).
                                                                                                                                                                                                                                                                                                                                                                                               BE1019159E65B2D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:| || || :| :: :| |: || 413 ASHEQAAIALKNAGQIVTIIAQYKPEEXSRFEAKIHDLR 451
                                                                                                                                                                                                                                                                                               GUANYLATE KINASE.
E -> V (IN REF. 3).
VIV -> EFR (IN REF. 4).
GDQ -> AGI (IN REF. 4).
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Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLG1_HUMAN STANDARD; PRT; 904 AA. 012959; Q12959; C12958; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 41, Last annotation update) Presynaptic protein SAP97 (Synapse-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Mismatches
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SWART; SM00072; GuKc; 1.
SWART; SM00326; PDZ; 3.
SWART; SM00326; SH3; 1.
PROSITE; PS000856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50002; SH3; 1.
SH3 domain; Repeat; 3D-structure.
DOMAIN
                                                                             Η;
                                                                                                                                                                       3D-structure.
194 PDZ 1.
289 PDZ 2.
436 PDZ 3.
541 SH3.
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83
401
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289
436
541
767
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81
399
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523. ASHEQAAAALKNAGQAVTIVAQYRPEEYSRFEAKIHDLREQMMNSSISSGSGSLRTSQKR 582
                                                                                062696
                                                        RESULT 11
                                                                DLG1_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                    EIPDDMGSKGLK -> QSFNDKRKKNLFSRKFPFYKNKDQS
EQETSDADQ (in isoform 2).
/FTId=VSP_003150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100354 MW; B78798D6BB0920D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.4%; Score 192; DB 1; 35.2%; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                     SH3.
GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                     PDZ
PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                              EMBL, U13897, AAA50599.1; -.
EMBL, U13896, AAA50598.1; -.
PIR, 138756, 138756.
PIR, 138757; 138757.
PDB, 1PDR, 23-JUL-97.
Genew, HGNC:2900; DLG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534
538
547
904 AA;
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Best Local Similarity
Matches 44; Conserv
                                                                                                             601014;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS. STMILARITY: CONTAINS 3 PDZ/DHR domains.
SIMILARITY: Contains 1 SH3 domain.
SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: IN CULTURED T84 CELLS, IT IS RESTRICTED TO THE CYTOPLASMIC SURFACE OF THE PLASMA MEMBRANES BETWEEN ADJACENT CELLS, BUT NOT AT THE EDGES OF CELLS LACKING CELL-CONTACT. TISSUE SPECIFICITY: PRESYNAPTIC NERVE TERMINI OF EXCITATORY SYNAPSES. IN OTHER BRAIN REGIONS, SAP97 IS FOUND IN AND ALONG BUNDLES OF UNMYELINATED AXONS. SAP97 IS NOT RESTRICTED TO THE CNS, BUT IS ALSO PRESENT AT THE BASAL LATERAL MEMBRANE BETWEEN A VARIETY OF EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mueller B.W., Kistner U., Veh R.W., Cases-Langhoff C., Becker B., Gundelfinger E.D., Garner C.C.; W., Cases-Langhoff C., Becker B., Gundelfinger E.D., Garner C.C.; and Saperated Construction of Sap97, a novel presynaptic protein homologous to Sap90 and the Drosophila discs-large tumor suppressor protein."; J. Neurosci. 15.2354-2366(1995).
-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPTOR SUBUNITS. MAY BE INVOLVED IN SYNAPTOGENESIS. MAY PLAY A ROLE IN CELL ADHESION.
                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Presynaptic protein SAP97 (Synapse-associated protein 97) (Discs,
                                                                                                                                            911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodom; PD000066; SH3; 1.
SMART; SM0072; GuKc; 1.
SMART; SM0050; L127; 1.
SMART; SM0050; L127; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS0056; GDANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U14950; AAA79976.1; -.
PIR; I56552; I56552.
HSSP; Q12959; IPDR.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR004172; L27.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95198112; PubMed-7891172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00625; Guanylate_kin; 1.
Pfam; PF00595; PDZ; 3.
                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequ
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
213 QLLIQ 217
                           583 SLYVR 587
                                                                                                                                                                                                                                                                large homolog 1).
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STRUCTURE BY NMR OF 1361-1456.
MEDLINE=20170882; PubMed=10704206;
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EMBL, D21209; BAA04750.1; --
EMBL, D21210; BAA04751.1; --
EMBL, X80289; CAA56563.1; --
EMBL, X78676; CAA56563.1; --
PIR, A54971; A54971.
PIR, I67639; I67629.
PIR, I67630; I67630.
PDB; JDSG; 24-JUL-02.
Genew; HGNC:9646; PTPN13.
MIM: 600267; --
                                                                                                                                                                                                                                                                                                  FETAL BRAIN.
                                                                                                                                                                                     PDZ domain.
                                                                                                                                                                                                                                                             Name=3;
                                                                                                                                                                                                                          Name=1;
                                                                                                                                                                                                                                            Name=2;
                                                                                                                       receptor.";
                                                              [9]
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                                                                                                                                          106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                    166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR-------TARRRQQQ 212
                                                                                                                                                                              522 ASHEQAAAALKNAGQAVIIVAQYRPEEYSRFEAKIHDLRETMMNSSVSGSGSLRISQKR 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.; "Cloning and characterization of PTPL1, a protein tyrosine phosphatase with similarities to cytoskeletal-associated proteins."; J. Biol. Chem. 269:24082-24089(1994).
                                                                                                                                                                                                                                                                    Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
"Molecular cloning of a novel protein-tyrosine phosphatase containing
a membrane-binding domain and GLGF repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Breast carcinoma;
MEDLINE-94350988; PubMed-8071359;
MEDLINE-94350988; PubMed S., Shen S.-H.;
Banville D., Ahmad S., Stocco R., Shen S.-H.;
"A novel protein tyrosine phosphatase with homology to both the cytoskeletal proteins of the band 4.1 family and junction-associated
                                                                                                             14; Gaps
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                        Length 911;
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang H.Y.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                         18CEBD31DD0CAF8B CRC64;
                                                                                         Score 192; DB 1;
Pred. No. 1.4e-06;
                                                      GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                              Mismatches
                                                                 POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 269:22320-22327(1994).
                 PDZ 1.
PDZ 2.
PDZ 3.
SH3.
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MEDLINE=95014139; Pubmed=7929060;
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MEDLINE=94116679; PubMed=8287977;
                                                                                                             23;
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                                                                         100570 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 337:200-206(1994).
                                                                                           16.4%;
35.2%;
PROSITE; PS50002; SH3; 1.
                                                                                                              44; Conservative
                                     545
650
911
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      guanylate kinases."
          Repeat
                                                                         911 AA;
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                          SLYVR 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                         213 QLLIQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Pancreas;
                                    465
         SH3 domain;
                                                                                                                                                 463
                                                                          SEQUENCE
                                                       DOMAIN
                                                                                                                                                                                                                                                     RESULT 12
PTND_HUMAN
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INTERACTION WITH TRIP6.

MEDLINE=99329089; PubMed=10400701;

Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.;

"ZRP-1, a zyxin-related protein, interacts with the second PDZ domain of the cytosolic protein tryrosine phosphatase hPTP1E.";

J. Biol. Chem. 274:20679-20687(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOId=012923-3; Sequence=VSP_000497;
TISSUE SPECIFICITY: PRESENT IN MOST TISSUES WITH THE EXCEPTION OF
THE LIVER AND SKELETAL MUSCLE. MOST ABUNDANT IN LUNG, KIDNEY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine + phosphate.
                                                                                                                                                                                                                                                                                                                                           Kozlov G., Gehring K., Ekiel I.; "Solution structure of the PD22 domain from human phosphatase hPTPlE and its interactions with C-terminal peptides from the Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 39:2572-2580(2000).
-!- FUNCTION: BINDS TO A NEGATIVE REGULATORY DOMAIN IN FAS THAT
- INHIBITS FAS-INDUCED APOPTOSIS.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Contains 5 PDZ/DHR domains.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000299; Band_4.1.
InterPro; IPR000299; Band_4.1.
InterPro; IPR0001478; PDZ.
InterPro; IPR0001478; PDZ.
InterPro; IPR000242; Tyr_PP.
Pfam; PF0073; Band_41; 1.
Pfam; PF00173; Band_41; 1.
Pfam; PF00105; PDZ; 5.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=3;
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SMART; SM0228; PD2; 5.
SMART; SM00194; PTPC; 1.
PROSITE; PS00660; FERM_1; FALSE_NEG.
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Cell Res. 11:223-229(2001).
                                                                                                                                                                                                                                                                                                                           Gene 294:99-99(2002).
                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                    PARD3 OR PAR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigens
                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform 3).
/FYIG=VED_1000497.
LD -> FH (IN REF. 3).
KDHHWSRGTLRHIS -> DLSRSHCHVYLAHL (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 VELPKTDEGLGFNVMGG -- - KEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                  GĽ -> A (IN REF. 4).
S -> P (IN REF. 4).
T -> RS (IN REF. 4).
T -> TVLFDK (IN REF. 1).
P -> A (IN REF. 3).
R -> K (IN REF. 3).
KSQEDDICTMEYYPQKI -> RVKKIPFVPCFTILRKR
                                                Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structure; Alternative splicing; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.4%; Score 169; DB 1; Length 2485; 28.4%; Pred. No. 0.00022; ive 26; Mismatches 43; Indels 3:
                                                                             PROTEIN-TYROSINE PHOSPHATASE.
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                   A -> S (IN REF. 4).
GLLDQ -> VARS (IN REF. 4).
                                                                                                                                                                             Missing (in isoform 2). /FIId=VSP_000496.
                                                                                                                                                                                                                                                                                         (IN REF. 4).

G -> A (IN REF. 3).

AA -> G (IN REF. 4).

A -> S (IN REF. 4).
                PDZ; 5.
TYR_PHOSPHATASE_1; FALSE_NEG.
TYR_PHOSPHATASE_2; 1.
TYR_PHOSPHATASE_PTP; 1.
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Missing (in is
                                                               POLY-LEU.
                                                                                                                                                             POLY-SER
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PDZ 2.
PDZ 3.
PDZ 4.
PDZ 5.
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        FERM 3;
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Best Local Similarity
              PROSITE; PS50106;
PROSITE; PS00383;
PROSITE; PS50056;
                                       PROSITE; PS50055;
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CONFLICT
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                                                                                                                                                                   ACT_SITE VARSPLIC
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Joberty G., Petersen C., Gao L., Macara I.G.; "The cell-polarity protein Par6 links Par3 and atypical protein kinase C to Cdc42.";
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S. .,
PAD3_HUMAN STANDARD;
PRT; 1356 AA.

QBTEM7; QBTEM7; QBTEM7; QBETS7;

QBTS6, QBTEM7; QBNXE6;

QBST58, QBHC48; QBNXE4; QBNXE6;

15-SEP-2003 (Rel. 42, Created)

15-SEP-2003 (Rel. 42, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordam H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina R., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6), INTERACTION WITH PARDEB AND PRKCZ, AND TISSUE SPECIFICITY.

PubMed=12234671;

Gao L., Macara I.G., Joberty G.;

"Multiple splice variants of Par3 and of a novel related gene, Par3L, produce proteins with different binding properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-Hepatoma, and Ovarian carcinoma;
Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Chiba T., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamanoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayamagi T.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Serological detection of cutaneous T-cell lymphoma-associated
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 3), AND INTERACTION WITH PARD6B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Testis;
BLDLINE-21143360; PubMed=11149944;
Elchmuellar S., Usener D., Dummer R., Stein A., Thiel D., Schadendorf D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A. (ISOFORMS 2; 3; 7; 8 AND 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 98:629-634(2001).
                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
MEDLINE=20394296; PubMed=10934474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell Biol. 2:531-539(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 857-1356 FROM N.A.
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Suzuki A., Yamanaka T., Hirose T., Manabe N., Mizuno K., Shimizu M.,
Suzuki A., Yamanaka T., Hirose T., Manabe N., Mizuno K., Shimizu M.,
Akimoto K., Izumi Y., Ohnioshi T., Ohno S.;
A Atimoto K., Izumi T., Ohnishi T., Ohno S.;
Tapithelia - specific junchional structures.";
Tell Biol. 153:1183-1196(2001).
Tell Biol. 153:1183-1196(2001).
Tell Biol. 153:1183-1196(2001).
Tell Biol. 153:1183-1196(2001).
The formation of epithelial tight junctions. Association with PARD6B may prevent the interaction of PARD3 with FILK/JAM.
Thereby preventing tight junction assembly. The PARD6 PARD3
Complex links GTP-bound Rho small GTPases to atypical protein kinase C proteins.
Thereby preventing tight junction assembly. The PARD6 PARD3
Complex links GTP-bound Rho small GTPases to atypical protein kinase C proteins.
Thereby preventing tight junction assembly. The PARD6 PARD3
Complex links GTP-bound Rho small GTPases to atypical protein kinase c proteins.
Thereby preventing tight junction assembly. The PARD6B PRKCI or PRKCZ and CDC42 or RACI. Interacts with PARD6A or PARD6B. PRKCI or PRKCZ and CDC42 or RACI. Interacts with PILK/JAMI (By similarity).
Complex and PRKCI at epithelial tight junctions.
Complex and PRKCI at epithelial tight junctions.
Complex and PRKCI at epithelial tight junctions.
Complex PATDERNATIVE PRODUCTS.
Complex PAT
                                   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Shevchenko Y., Boutfard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human.
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=8; Synonyms=Sa;
IsoId=Q8TEW0-8; Sequence=VSP_007464, VSP_007470, VSP_007471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSCALG-XCALD...
Name=9; Synonyms=Sb;
ISOId=Q&TEW0-9; Sequence=VSP_007463, VSP_007464, VSP_007465,

VSP_007470, VSP_007471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q@TEWO-5; Sequence=VSP_007462, VSP_007463, VSP_007464,
VSP_007466, VSP_007468, VSP_007469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnnsson A.-S., Driessens M., Aspenstroem P.; "The mammalian homologue of the Caenorhabditis elegans polarity protein PAR-6 is a binding partner for the Rho GTPases Cdc42 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT OF A COMPLEX CONTAINING PARD6B AND PRKCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                me=2; Synonyms=B, La;
IsoId=Q8TEW0-2; Sequence=VSP_007464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSP_007465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1; Synonyms=A;
IsoId=Q8TEW0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell sci. 113:3267-3275(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH PARD6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=4; Synonyms=D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synonyms=C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synonyms=E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10954424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=5;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 ARATAKATVAAFAASEGHSHPRV----VELPKTDEGLGFNV-----MGGKEQNSPIYI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FIId-VSP_007463.
Missing (in isoform 2, isoform 3, isoform 5, isoform 6, isoform 7, isoform 8, isoform 9 and isoform 10).
/FIIG-VSP_007464.
Missing (in isoform 3, isoform 6, isoform 7, isoform 9 and isoform 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform 3, isoform 5, isoform 6, isoform 7 and isoform 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Indels 16; Gaps
TISSUE SPECIFICITY: Widely expressed.

PTM: Phosphorylated by PRKCZ.

MISCELLANEOUS: Antibodies against PARD3 are present in sera from patients with cutaneous T-cell lymphomas.

SIMILARITY: Belongs to the PAR3 family.

SIMILARITY: Contains 3 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLLED COIL (POTENTIAL).
PHOSPHOPNIALTY).
PHOSING (in isoform 3 and isoform 5).
/FIId-VSP_007462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDZ 3.
INTERACTS WITH PRKC2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                             DIGETTA: PF00555; PDZ; 3.
SWART; SM00228; PDZ; 3.
SWART; SM00228; PDZ; 3.
Cell Gycle; Cell division; Tight junction; Membrane; Repeat; Colled coil; Phosphorylation; Alternative splicing; Polymorphism. DOMAIN 271 359 PDZ 1.
DOMAIN 461 F46 PDZ 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 167; DB 1; Length 1356; Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COILED COIL (POTENTIAL).
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COIL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYS-RICH.
                                                                                                                                                                                                                                                                                                                                                  AK027735; BAB55330.1; ALT_INIT.
AF177228; AAG33676.1; ALT_TERM.
BC011711; AAH11711.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                         AK000761; BAA91366.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COILED
                                                                                                                                                                                                      EMBL; AF252293; AAF71530.1; -.
EMBL; AF196185; AAK27891.1; -.
EMBL; AF196186; AAK27892.1; -.
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36.08;
                                                                                                                                                                                                                                                AAK69192.1;
                                                                                                                                                                                                                                                           AAK69193.1;
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                                                                                                                                                                                                                                                                                   AF467003; AAL76043.1;
AF467004; AAL76044.1;
AF467005; AAL76045.1;
AF467006; AAL76046.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.3
Best Local Similarity 36.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                           HGNC:16051; PARD3
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936
1042
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1174
1224
1301
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238
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                                                                                                                                                                                                                                                                        AF467002;
AF467003;
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1201
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MIM; 606745;
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VARSPLIC
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RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                                                 Joberty G., Petersen C., Gao L., Macara I.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pawson T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interacts with FIIR/JAMI.

Substituting Localized Substitution Cytoplasmic; membrane associated. Localized along the cell-cell contact region. Colocalizes with PARD6A and PRKCI at epithelial tight junctions.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), SUBCELLULAR LOCATION, PHOSPHORYLATION BY PRKCZ, INTERACTION WITH PRKCI AND PARD6A, SUBUNIT OF A COMPLEX CONTAINING PARD6A AND CDC42, AND MUTAGENESIS OF
                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH PARDSB, AND SUBUNIT OF A COMPLEX CONTAINING PARDSB
                                                                                                                                                                                                  Lin D., Gish G.D., Songyang Z., Pawson T.; "The carboxyl terminus of B class ephrins constitutes a PDZ domain binding motif.";
                                                                                                                                                                                                                                                                                                              MEDLINE-20394297; PubMed-10934475; Mbamalu G., Scott J.D., Pawson Lin D., Radvards A.S., Fawcett J.P., Mbamalu G., Scott J.D., Pawson "A mammalian PAR-3-PAR-6 complex implicated in Cdc42/Rac1 and aPKC signalling and cell polarity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly of epithelial tight junctions is negatively regulated by
                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                              15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Partitioning-defective 3 homolog (RARD-3) (PARC-3) (Atypical PKC isotype-specific interacting protein) (ASIP) (Ephrin interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11447115;
Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.;
"The cell polarity protein ASIP/PAR-3 directly associates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS:
Event-Alternative spliting; Named isoforms=3;
Name-1; Synonyms=180 kDa;
Isold=099NH2-1; Sequence-Displayed;
Name=2; Synonyms=150 kDa;
           PRT; 1333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               junctional adhesion molecule (JAM).";
EMBO J. 20:3738-3748(2001).
                                                                                                                                                                                                                                  J. Biol. Chem. 274:3726-3733(1999).
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20394296; PubMed=10934474;
                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 3).
STRAIN-NIH Swiss; TISSUE-Embryo;
MEDLINE-99121117; PubMed-9920925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERACTION WITH FILR AND PARD6B. PubMed=11839275;
                                                                                                                                                                                                                                                                                                                                                           Nat. Cell Biol. 2:540-547(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gao L., Joberty G., Macara I.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Cell Biol. 2:531-539(2000).
            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH FILE.
                                                                                                                                                                                                                                                                                                    STRAIN-NIH Swiss;
                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                          824-SER--SER-826
                                                                                       protein) (PHIP).
PARD3 OR PAR3.
                                                                                                                                                                                                                                                                                                                                                                                              PRKCI AND CDC42.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Cdc42
            PAD3 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                         C to
PAD3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VELPKIDEGLGFNV-----MGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 IQLKKGTEGLGFSITSRDVTIGG---SAPIYVKNILPRGAAIQDGRLKAGDRLIEVNGVD 518
                 Name-3; Synonyms-100 kDa;
Isold=099NH2-3; Sequence=vSP_007472, VSP_007473;
Isold=099NH2-3; Sequence=vSP_007472, VSP_007473;
IISOUS SPECIFICITY: All isoforms are expressed in heart, while expression in brain is mainly limited to isoform 1, and to isoform 3 to a weaker level.

DEVELOPMENTAL STAGE: Isoforms 1 and isoform 3 are expressed from E 9.5 to E14.5, while isoform 2 is not expressed.

PTM: Phosphorylated by PRKC2.

SIMILARITY: Contains 3 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 VEGEHHEKAVELLKAAK--DSVKLVV----RYTPKVLEEMEARFEKLRTARRRQQQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Partitioning-defective 3 homolog (PARD-3) (PAR-3) (Atypical PKC isotype-specific interacting protein) (ASIP) (Atypical PKC specific binding protein) (ASBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMS->AMA, EME: STRONGLY REDUCES
PHOSPHORYLATION BY PRKCZ AND ABOLISHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTS WITH PRKCZ (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.8%; Score 161.5; DB 1; Length 1333; 34.2%; Pred. No. 0.00036; ive 27; Mismatches 31; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY).

KCOL -> ESGT (in isoform 3).

FTIG-VSP_007472.

Missing (in isoform 3).

FTIG-VSP_007473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SMUULZE; rus, ...
PROSITE; PSSOLO6; PDZ; 3.
PROSITE; PSSOLO6; PDZ; 3.
PDZ; 3.
Colled coi; Plosphorylation; Alternative splicing.
DOMAIN 271 359 PDZ 1.
DOMAIN 461 546 PDZ 2.
TOWNER 590 677 PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH PKRCI.
1333 AA; 149060 MW; AF67825C66DCFE86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYS-RICH.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform 2). /FTId=VSP_007474.
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COILED COIL (POTENTIAL)
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IsoId=Q99NH2-2; Sequence=VSP_007474;
me=3; Synonyms=100 kDa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AY026057; AAK07669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:2135608; Pard3.
InterPro; IPR001478; PD2.
Pfam; PF00595; PDZ; 3.
SMARI; SM00228; PDZ; 3.
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PDZ 2. PDZ 3. INTERACTS WITH PRKCZ (PROBABLE).

LYS-RICH. COILED COIL (POTENTIAL)

(POTENTIAL) COIL (POTENTIAL)

COILED COIL

546 677 936 1042 1172 1222 1229 1299

1149

827 1034 1337

1278

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoda-092340-2; Sequence-VSP_007475;
-!-TISSUE SPECIFICITY: Isoform 1 is predominently expressed in lung, glandular stomach, prostate, ovary and uterus. Isoform 1 is also expressed in brain, with a high expression in the cortex, hippocampus and in the striatum. Isoform 2 is predominently expressed in intestinal epithelial cells, kidney and prostate.
-!- PTM: Phosphorylated by PRKCZ (By similarity). The phosphorylated form is concentrated at the most apical tip of cell-cell contacts during the initial phase of tight junction formation.
-!- SIMILARITY: Belongs to the PAR3 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB005549; BAA34216.1; -.
PIR; T13948; T13948.
HSSP; Q12023; 3PD2.
InterPro; IPR001478; PD2.
Pfam; PR00595; PD2; 3.
SMART; SM00228; PD2; 3.
PROSITE; PS50106; PD2; 3.
Cell cycle; Cell division; Tight junction; Membrane; Repeat; Coiled coil; Phosphorylation; Alternative splicing.
DOMAIN 271 359 PD2 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=180 kDa;
IsoId=Q92340-1; Sequence=Displayed;
Name=2; Synonyms=150 kDa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                   Rattus norvegicus (Rat).
                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --
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Local Similarity 31.0 nes 45; Conservative DOMAIN MOD\_RES VARSPLIC SEQUENCE Query Match DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN Best Loc Matches δŽ d δŏ Ω δŽ Kinase C proteins.
SUBUNIT: Interacts with PARD6A, PARD6B and FILK/JAMI via its PD2 1
domain (By similarity). Interacts with PRKCI. Interacts with PRKCZ
(Probable). Part of a complex with PARD6A or PARD6B, PRKCI or
PRKCZ and CDC42 or RACI (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic; membrane associated. Localized
along the cell-cell contact region. Colocalizes with PRKCZ at the
ALTERNATIVE PRODUCTS: Izumi Y., Hirose T., Tamai Y., Hirai S.-I., Nagashima Y., Fujimoto T., Tabuse Y., Kemphues K.J., Ohno S.;
"An atypical PKC directly associates and colocalizes at the epithelial tight junction with ASIP, a mammalian homologue of caenorhabditis elegans polarity protein PAR:3";
J. Cell Biol. 143:95-106(1998). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH PRKCI AND PRKCZ division junction formation.";
J. Cell Sci. 115:2485-2495(2002).
J. Cell Sci. 115:2486-2495(2002).
Add Cell Polarization processes. Seems to play a central role the formation of epithelial tight junctions. Association with PARD6B may prevent the interaction of PARD3 with FILK/JAM1, thereby preventing tight junction assembly. The PARD6-PARD3 complex links GTP-bound Rho small GTPases to atypical protein Hirose T., Izumi Y., Nagashima Y., Tamai-Nagai Y., Kurihara H., Sakai T., Suzuki Y., Yamanaka T., Suzuki A., Mizuno K., Ohno S., "Involvement of ASIP/PAR-3 in the promotion of epithelial tight SEQUENCE FROM N.A. (ISOFORM 2), SUBCELLULAR LOCATION, AND PHOSPHORYLATION OF SER-827. PubMed=12045219; TISSUE=Fibroblast; MEDLINE~98437350; PubMed=9763423;

9

24; Gaps

Length 1337; 44; Indels

; DB 1; 0.00039;

Score 161; No.

Pred.

13.8%;

32; Mismatches

149448 MW; EC980C5106B52F9C CRC64; Missing (in isoform 2). /FTId=VSP\_007475.

AA;

COILED COIL (POTENTIAL) PHOSPHORYLATION.

Search completed: September 23, 2003, 15:14:11 Job time : 14 secs

188 YTPKVLEEMEARFEKLRTARRQQQ 212 551 FHPR---EMNAEPSQMQSPKETKAE

135 SRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAK--DSVKLVV----R 187